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(without alignments) 2756.533 Million cell updates/sec 1 PGRPTRPKAPSHSAPLLGLA......LQSWVPEMQDPQSWKGKEGT 1416 Gapop 10.0 , Gapext 0.5 US-09-836-712-2 BLOSUM62 Perfect score: Scoring table: Sequence: Title:

283366 Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

piri: PIR 78:* Database

Fred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		-			SUMMARIES	
90	GOL	ate	Lengt	DB	ID	scription
-		14.4	2165		T21371	hypothetical
2	95	12.3	1205		51	procellagen N
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12	428.5	5.5	860		6	hypothetical
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14	275	3.5	788		9	hypothetical
15	264.5	3.4	1584		2	brain-specifi
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ALIGNMENTS

RESULT 1

hypothetical protein F25H8.3 - Caenorhabditis elegans	CiSpecies: Caenorhabditis elegans Cipate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 29-0ct-1999 Ciancesion: T2171: T24896
hypothetical protein F2	CySpecies: Caenorhabditis e. CyDate: 15-Oct-1999 #sequenc

A,Status: preliminary; translated from GB/EMBL/DDBJ R,Gajadsty, S. Submitted to the EMBL Data Library, February 1996 A,Reference number: 219413 A,Recession: T21371 A;Molecule type: DNA A;Residues: 1-2165 <WIL>

A,Cross-references: EMBL: Z69360; PIDN: CAA93287.1; GSPDB: GN00022; CESP: F25H8.3 R.jdajadsty, S. aubmitted to the EMBL Data Library, February 1996 A.Reference number 219949 A.Accession: T24896 A, Experimental source: clone F25H8

A.Crose-references: BMEL:259561, PIDN:CAA93288.1; GSPDB:GN00022; CESP:P2588.3 A.Raperiental source: clone T13810 (Centelos: A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A:Gene: CESP: F25H8.3

A.Map position: 4 A.Introns: 31/1, 52/1, 135/2, 193/3; 216/1; 266/1, 495/2, 547/3; 584/3; 634/2; 744/1; 42 Query Match 14.4%; Score 1118; DB 2; Length 2165; Sepset Local, Similarity 26.6%; Pred. No. Le-62; Most Local, Stall Conservative 142; Mismatches 501; Indels 272; Gaps Matches 311; Conservative 142; Mismatches 501; Indels 272; Gaps

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91 GRORGRRAAGGILH-LELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAGFRV 149 150 HIVKAVILTEPEGAPNITANLISSLLSVÇGMSQTINPEDDIDEGHADLVLYITRFDLELP 209 327 VVVKLIVLKTENAGPRITONAQOTLODPCRWOQYYNDPDDSSVOHHDVALLLTRKDICRS 386 387 QCCDTLGLARLGTMCDMQKSCAIIBDNGLSAAFTIAHBLGHVFSIPHDDE--RKCSTYM 444 268 -------SGHVMASDGAAPRAGLAMSPCSRRQLLSLL--SAGRARCV 305 445 PVNKVCKFOSTKFDKTQFQNNFHIMAPTLEYNTHEWSWSPCSAGMLERFLENNRGQTQCL 504 306 WDPPRPQPGSAGHPPDA----OPGLYYSANBQCRVAFGPKAVACTFAREHLDMCQALSCH 361 267 RKARSRRAANSWDHYVEVLVVADTXMYEYHGRSLEDYVLTLFSTVASIYRHOSLRASINV 326 210 DONRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAFGSGCGP--윱 윱 ò à 9 ઠે g

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956 IDCSTRWITEDV-SSCSAKCGSGQKRQRVSCVKWEGDRQTPASEHLCDRNSKPSDIASCY 1014
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                                                                                                   PCSRSCGGGWVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLEFMSQQCARTD 477
                                                                                                                                                  514 ECSRICGGGVQKGLRDCDSPKPRNGGKYCVGQRERYRSCNIGECPWDIQPYREVQCSEFN 673
                                                                                                                                                                                                      178 GOFLRSSFGGASFYHWGAAVPHSQGDALCRHWCRAIGESFIMKRGDSFLDGTRCMPSGFR 537
                                                                                                                                                                                                                                                                                                          538 EDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAREYVTFL 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S---GSDAI--IERINGTGPIRSDIYVHVL----SVGS-HPPDISYEYMTAAVPNAVIR 895
                                                    TEYGSOMGCRIOHMPWADGIPCDESRSMFCHHGAC---VRLAPESLIKIDGOMGDWRSWG 613
                                                                                                                                                                                                                                                                                                                                                    -----DICVAGACMPAGCDHQLHSTLRRDKCGVCGGDDSSCKVVKGTFNEQGTFGYNEVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNPOPCPARMEVSEPSSCTSAGGAGLALENETCVPGADGLEAPVTEGFGSVDEKLPAPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTRGSEG--TIVDEYPCDRNTRPRIKKTCEKDTCDGPRVIOKLOADVPPIRWATGPWTAC
                                                                                                                                                                                                                                      598 TVTPNLTSVYIA----NHRPLFTHLAVR-IGGRYVVAGKOKSISPNTTYPSLLEDGRVEY
TDPLDQSSCSRLLVPLLDGTECGVEK--WCSKGRCRSLVELTP--IAAVHGRWSSWGPRS
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procollagen N-endopsptidase (SC 3.4.24.14) I - bovine
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A:Description: catalyzes cleavage of the propeptides of type I and II collagens prior C.Keywords: hydrolase; metalloproteinase
R. Richiste, A. Mangana, B. V. Ladabree, C. P. Zabrasay, 1996
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Phychesters process NAAA0669 - human process N
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A:Residuce 1.837 vones : RMBL:AB014589; NID:g3327189; PIDN:BAA31663.1; PID:g3327190
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87 GASFYHWGAAVPHSQGDALCRHMCRAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCV 546
                                                                                                                                                                                                                                                                                       47 SGSCRIFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRARBYVTFLTVTFNLTSV 606
                                                                                                                                           23 NEPTVEWTPKYAGVSPKDRCKLTCEAKGIGYFFVLQPKVVDGTPCSP----DST-SVCV
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9.6%; Score 746.5; DB 2, Length 837;
Best Local Smilarity 30.6%; Pecel No. 1.46-29;
Matches 211; Conservative 92; Wismatches 300; Indele 83;
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C. Superfamily: thrombospondin type 1 repeat homology
F:519-751/Domain: thrombospondin type 1 repeat homology «THR3»
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; Cross-references: RMBL-ABG01735; NID:g2809056; PIDN:BAA24501.1; PID:g2809057
; EXpestimental Bontres: strain 1298VJ
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                                                                                  428 VIRREQCHAPPAFGGRACVGADLQAEMCNIQAC-EKIQLEFMSQQCARIDGQPLRSSPG 486
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               1059 -----SVAC------VQLDQGQDVBVDBAACAALVRPEASVPCLIAD 1094
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C.§Species: Mus matechlus (house mouse)
C.Date: 22-04n-1199 Hacquence_revision 22-04n-1999 #text_change 21-Uul-2000
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See Local Similarity 3014, Pred, No. 4.2e-52, Indels 117; Gaps Marches 34; Indels 117; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Introns: 228/1; 343/3; 388/1; 444/1; 539/3; 602/1; 660/3; 719/2
Superfamily: thrombospondin type I repear homology (FIRS)
542-58/Domain: thrombospondin type I repear homology (FIRS)
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Molecule type: Dan.
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                                                                                                                                                                                                                                                                                                          565 RPRSCWIEDCPIGSALIFREEQCAAYNHRID -- LFKSFPGPMDWVPRYIGVAPQDQCKLI 622
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                                                VAPGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRCR 395
                                                                                                                                                                                                        108 HMDQLQDFNIPQA---GGWGPWGPWGPWGDCSRTCGGGVQFSSRDCTRPVPRNGGKYCEGRRT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DROGVOGGDNSTOSPRKGSFTAGRAREYVTFLTVTPNLTSVYI-----ANHRPLFTHLAV
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95 MAHYDPEEPWSPCSARFIIDPLDNGYGHCLLD----KPRAPLHLPVTFPGXDYDADROCO
                                                                                                       151 LIFGFDSRHCP---QLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAGACMGGRCL
                                                                                                                                                                                                                                                                                                                                                                 CRHMCRAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVW
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Physiotherical process no RESCACLISto. 1 - Numen (response):
Classical Homos separate (Ran)
C

A;Cross-references: EMBL:AL162080 A;Experimental source: adult melanoma (MeWo cell line); clone DKFZp762C1110 A/Status: preliminary A/Molecule type: mRNA A/Residues: 1-550 cAAA>

Note: DKFZp762C1110.1 C.Genetics:

263 SGCGPSGHVMAS-----DGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQPGSAG 317 318 HP---PDAQPGLYYSANEQCRVARGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLL 374 4 NGVNQDSHMMASMLSNLDHSQP-----WSPCSAYMITSPLDNGHGECLMDKPQ-----Guery March 18 Sect Local Similarity 30.4% Pred No. 1.6e-35; Indels 118, Gaps Marches 185, Conservative 75; Mismarches 331, Indels 118, Gaps

52 NPIQLPGDLPGTSYDANRQCOPTFGBDSKHCPDA---ASTCSTLWCTGTSGGVLVCOTKH 108

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408 GRWSSWGPRSPCSRSCGGGVVTRRROCNNPRPAFGGRACVGADLOAEMCNTOACEKTOLE 467 Gaps Indels 237; Query Match 85% Score 659.5; DB 2; Length 1558; Ber Local Similarity 24,9%; Pred. No. 916-34; D. 1634; Matches 339; Conservative 106; Mismatches 379; Indels 237; ò

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337 LEBEVDYMYKFDNWT----PCSVSCGKGVOTRNLYCIDGKNKGRVBDDLCBRNNATKPBF 392

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Gaps

Indels 273; Length 951;

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Althor Frederico of the Goodle sequences of unidentified human gones. IN. The Agreement number: 12.408 WILD 928285811 Applies the Committee of the Committee of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 TQLEFMSQQCARTDGQPLRSSPGGASFYHWGAAVP----HSQGDALCRHMCRAIGESFIM 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 DGRSFREEGCV----SPNSHVYNGRTHQWKPLYPDDYVHISSKPCDLHCTTVDGGRQLM 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 VPA---RDGTSCKLTDLR----GVCVSGKCEPIGCDGVLFSTHTLDKCGICQGDGSSCT 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        520 XRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         690 NLTRPDITFTY--FQP----KPRQAWVMANVRGFCSVSCGAGL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARCRAGAOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
7.1%; Score 546.5; DB 2;
Best Local Similarity 2.2%; Pred. No. 7.8e-27;
Metchee 216; Conservative 105; Mismatches 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                  A.Gene: CESP.PS186.2
A.Intropa position:
A.Intropa (18/3, 92/3, 131/3, 169/1, 236/2, 282/3, 349/2, 376/2, 420/1, 576/3, 759/3, 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
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Cibaco (1-26-1999 sapisma (raal)
Cibaco (1-26-1999 sequence_revision (11-Reb-1999 #text_change 21-301-2000
Ribageacon (1005)
Ribageacon (11-261)
Wib Res 5, 31-39, 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    968 VCQAVPCPARWQY-KLAACSVSCGRGVVRRILYCARAHGEDDGEEILLDTQCGGLPR-PE 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1026 POBACSLEPCFFRWKYMSLGPCSASCGLGTARRSVACVQLDQGQDVEVDEAACAALV--- 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .083 -----RPEASVPCLIADCTYRW------HVGTWMECSVSCGDGIORRRD 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 --TCSSTCGTGVMSRTVECVAVNPISSAPIKLPMSECODOEOPKLPESCEVRSCPLOEDS 441
                                                                                                                                                                                                                                                                                                                                                                                  403 IAAVHG---RWSSWGPRSPCSRSCGGGVVTRRROCNNPRPAFGGRACVGADLOAEMCNTO 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460 ACEXTQLEFMSQQCARTDGQPLRSSPGGASFYHWGAAVPHSQGDALCRHMCRAIGESFIM 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 TCESKSRLARDTIC------GGEEI----VSRGOCEVVCR-SRLTGANFLW 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   520 KRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCS 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 -RVD---DGTPCQAATSR----AVCSKGSCQIVGCDGLISSSPRFDACGVCGGRGDTCD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 PRKGSFTAGRARBYVTFLTVTPNLTSVYIANHRPLFTHLAVRIGGRYVVAGKMSISPNTT 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540 YPSILEDGRUEYRVALTEDRIPRIEEIRIMGPLQEDADIQVYRRYGEEYGNLTRPDITFT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   748 QGSQQPPAMPEACVLEPCPPYMAVGDFGPCSASCGGGLRERPVRCVEAQGSLLKTLPPAR 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 ADKLRPKVEARPCPMLICPSRWMAADWTECVPHCGEGTRKREVYCVQTAHNVTVHVPDTF 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRAGAQQPAVALETCNPQPCPARWEVSEPSSCTSAGGAGLALENETCVPGADGLEAPVTE 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 CENGT-RPA-ABBNCVSTSC-GRWBAGKWSKCTASCGOGVRRRHVACVGGSDCDBG---- 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRPROETTCYAGIPCSIATNSLDWNDRAYLDGNTFGSMDNHNDWQAPRL---VAGEWS-- 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    924 AGSCSVSCGRGLMELRFLCM-----DSALRVPVQE------ELCGLASKPGSRRE 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        553 DRCHFKKPQETETCNVVACPATWVSSLNKRHNKIXLNKLKTAQWTEČŠRSČDSGERRRQV 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 IASPHVDALSWAAMSPWSSCTKTCGGGVSRQLRRCLTSK-----CSGBSVRFKVCAQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VOO YFOPKPROAWWAAVEGPCSVSC-----GAGLRHVNYS-----CLDOARKELVETVOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TACASMCDDIVDWSGAGRSIASTSQPIVVCVNAITGRVVPEKLC
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                                                                                                                                                                                                  al Statistity 23.9%; Proce 568; DB 2; Length 1059; all Statistity 23.9%; Prod. No. 3.80-28; Indels 248; 195; Conservative 81; Mismatches 292; Indels 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1121 TCLGPQAQAPV---PADFCQHLPKPVTVRGCWAGPC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        613 WCEIRDSRGKTQRRPDVBCDANTKPQTVEVCSFGSC 648
                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                           Duery Match
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Matches
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ò	JOINMECSVSCGDO	ò	584 SFTAGRAREYVTFLTVTPNLTSVYIANNRRPLFTHLAVRIGGRYVVAGKOKSISPNTTYPSL 643
Dp	831 TRSGPECGLAKKPPEESTCFERPC-PKMYTSPWSECTKTCGVGVPMRDVKCYQGTD 885	q	594pltbQss8vRsQ
è	1132 PADPCQHLPKPVTVRGCWAGPCVGQGTPSLVPHEEAAAPGRTTATPAGACGRQHLEPTGT 1191	λō	644 LEDGRVEYRVALTEDRLPRLEEIRINGPLQEDADIQVYRRYGEEYGNLTRPDITFTYFQP 703
Q	886 IVRGCDPLVKPVGRQACDLQPC912PPDDSCQDQ 919	qq	607
è	1192 IDWRGPGQADCAVAI 1206	65	704 KPRQAM-VWAAVRGPCSVSCGAGLRHVNYSCLDQARKELVETVQCGGSQQPPAMPEACVL 762
g	920PG-TWCALAI 928	g	609TWSLWISCTAICGGGYRKRARACSITGCCEGNEDETEVCSS 649
	:	È	763 EPCPPYMANG BPGPCSASCGGGIRERPVRCVEAQGSLLKTLP 804
T15976	111	음	650 ESCPSVLRVGNEWSTWIEMNHCSVSCGRGSQARYRKCLSPHRTLAFDCPGENKVTNELRI 709
C.Speci	Aypornetidal protein Posto.1 - Caenormabolils elegans C.Species: Caenorhabolils alegans C.Dete: 20-6sp-1999 #secuence retision 20-5sp-1999 #text chance 20-5ep-1999	è	805RWEVSEPSSCTS 841
C,Acces	ston: 715976	쉽	710 TFFKARSYIMCSVRCNKIKRNTISEKNIEVRSCDNGFCNAIGVWGTWGGWSTCST 764
Submitt A,Descr	n.,v.,v.,v.,v.,v.,v.,v.,v.,v.,v.,v.,v.,v.	à i	842 AGGAGLALENETOVPGALDGLEAPVTEGPGSVDEXLPAPEPCVGMSCPPGWGHLDA 896
A;Refer A;Acces	ence number: 218440 sion: T15976	g ;	765 SCGPGTLVRQRLC
A;Statt. A;Molec	s: preliminary; translated from GB/EMBL/DDBJ ule type: DNA	ŝ	200 CONTROL OF COLORS OF C
A,Resid A,Cross	.ues: 1-957 <ben> -references: EMBL:U29378; NID:g868184; PID:g868185; PIDN:AAA68721.1; CESP:F08C6.1</ben>	qq	796 TCCNDGIMSLWNEWSDCSRVCGKGLRSRSRSCFGSGC 832
A/Experiment C/Genetics:	imental source: strain Bristol N2	ò	957 GLASKPGSRREVCGAVPCPARMOYKLAACSVSCGRGVVKKLITCARAHGE 1005
A. Intro	A.Gene: CBSP:PO8C6.1 A.Introns: 23/1: 135/3: 220/3: 285/3: 325/2: 376/3: 461/2: 498/3: 532/3: 627/2: 714/1: 7	q	833 MGASSEQQFCNEQACASSSANDWGTKSGWSQCSVSCGAGVKRRTRTCRTGN 883
Onerv	Match 5.7%: Score 440: DB 2: Length 957:	ò	1007 DDGEEILLDTQCQGLFRFEFQEACSLEFCPPRWKVMSLGFCSASCGLGTARRSVACVQLD 1066
Match	Best Local Similarity 19.0%; Pred. No. 4.58-20, Matches 216; Conservative 99; Mismatches 299; Indels 524; Gans 46;	g	884GNYKESAIC 894
2	GPDVPOAHORDTERYVLTNINIGAELLEDPSLGAG	ò	1067 GGQDVEVDBAACAALVRPBASVPCLIADCTYRHHVGTWMECSVSCGDGIQRRRDTCLG 1124
. A	211 QRLTQQSDLIVELAVEVDENIWRHFSSKHGGWADRKLQDYTLTLANNIQIMYTQPTASPP 270	a	895 NDRDCENKOZÁMGG
ò	147 PRVHLVKAVILT-EPEGAPNITANLTSSLLSVÇGMSQTINPEDDTDPGHADLVLYIT 202	RESULT 12	2
Q.	271 LITERVIRYEVLIRQPSALAGYLHNHGNAQMYLDRFCRYQRNLAVRDWDHAIMLT 324	hypothet	ical protein T19D2.1 - Caenorhabditis elegans
ò	203 RFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPG 262	C,Date:	C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
DB	325 GYDIHRGAGSRSISGIARLDGMCDPMNTCTLAEGLDFTSAFIGTHELGHRF 375	R,Bentle	Structure of the PART Data Library. December 1995
ò	263 SGCGPSGHVMASDGAAPRAGLAWSPCSRRQLLSLLSAGRARCVMDPPRPQPGSAGHPPDA 322	A Descri	Appearing to the property of C. elegans cosmid T19D2. A.Reference number: Z18D9
e e	376	A, Access	A.Accession: T16892 A.Status: preliminary: translated from GB/ENBL/DDBJ
ò	323 QPGLYYSANEQCRVAPGPXAVACTFAREHLDWCQALSCHTDPLDQSSCSRLLVPLLDGTE 382	A, Residu	A. Molecule type: DNA A. Residues: 1-860 <ben></ben>
QC O	376IPTGTF 391	A;Cross-ref	A;Cross-references: EMBL:U42846; NID:g1125809; PID:g1125810; PIDN:AAA83600.1; CBSF:T191 C;Genetics:
òi	383 CQVEKWCSKQRCRQLVELTPIAAVHGRMSSWGPRSPCSR-SCGG- 425	A, Gene:	AjGene: CBSP:T19D2.1 AjIntrone: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; !
9 8	592 CURSANCULARCUPATURE QUI VARARAVATILES RELICERS SANS-ALICEGALICA 450 426GVUTRIR QCRIPPR PARFORM PURALONE MONTONCERTOLE PRISOCORFT 476	Query Best L	Query Match 5.5% Score 428.5, DB 2; Length 860; Bart Local Similatity 19.8%; Ped. No. 2.24-19. Response 21: Compound 10. Ped. Mo. 2.24-19.
DP	451 LGSVGLAIARRTCSAPYPANGGSDCVGSTSRAVLGSRQCGRASKSVDEYISDKCMEQKRL 510		r dudina
ò		s a	123 RRAEPHRR.—-DILTVELAVPRADDAMMOHFXXXVGKAABBNRHTFINAVNNNDVLYTOR 179
g	511 KNDRELTGKGSQLNREPGRACKVFC-DVQQHYGSQRNYREPGD 552	ò	142 SIGAGFRVHLVRAVILTEPEGAPNITANLISSLLSVCGWSQTINPEDDTDPGH 194
ે ક	524 SPLDGTRCMPSGPREDGTLSLCVSGSCRTPGCDGRNDSQQVMDRCQVCGGDXSTCSFRKG 583	eg G	180 LLQPRINIKIVRYELLKNIFHLMARKHSKNGDVDRLLDAFCQYQNEINPRNDADPRH 236
3		ò	195 ADLVLYITRFDLELPDGNRQVRGVTQLGGACSFTWSCLITEDTGFDLGVTIAMEIGHSFG 254

8 8	33	DRALLESGYDLH-RNOVKTVAGYAPVKGMCSGVESCTINEGLEPGSVPVTHEMGHSLG	0. 0
è 8	3 - E	SHDGDNE	96
oy gp	299 AV	MAGRARCYMDERROPGOSAGHEPDAOPGLYYSANBOCRVAPGPKAVACTFARBHLD 3 FREPRICLOGASANBORNYAFXESEREPORTLEPOGETFUBGOETFOR	153
è q	354 -	-MCGALSCHIDPLOGSSCSRLLVPLLDGTEGVPKACSKGRGRSLVELFPLAAVHGRNSS 4.	112
è 8	413 %	WOPRSPCSRSCGGGUVTRRROCNWPRPAFGGRACVGADLQAEMCHTGAC 4 WINDR	161
& e	462 E	BETOLE-PMSOCCARTDGOPLESSPOOASFYHKGANVPHSOGDALCRINGRA S 	512
% a	13	TIMIRGIDSFLOOTROMPSGPREDGTLSLCVSGSCRTFGCDGRADSQQVMDRCQVCG	
<u>ن</u> د	573 G	ONSTCS PREGGETAGRARE YVTELTVT ENLIS WYTARER BLFTHLAVRIGGRYVVAGEM RTTLANGES DE BENT BLAGES DE BEN	632
1 6 6	m 0	SENTITY PSILEDGRVEYRVALTEDRIPREDRIERING PLOSEDADIQVYRRYGESYGNITTY OF THE PSILEDGRAPH OF T	2 2 2
· > 8	6 8	PDITFTYPOPKPRCANVMAAVRGPCSVSCGAGLRHVNYSCLDDARKELVETVQCOG	74.9
ें ह	750 8	QQPPAWPEACV1EECPPYWAVGDFGBCSASCGGGIRERPVRCVEAGGSL1.KTLPPARCR - IAAVCAGARRE	
<i>ò</i> 8	9 5	SAQOPAVALETCNPOPCPARMEVSEPSSCTSAGGAGIALENETCVPGALGLEAPVTEGP	
\ & &	0 9	SUDEK	
è 8	4 1-	SCCRGIMBLRFLCMDSALRVPVQEELCGLAGKPGSRBVCGAVPCFGATCGAVPCFGATCGAVPCFGATCGAVPCFGATC	F 40
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T14764 hypotherical C;Species: Ho C;Date: 20-Se C;Accession: C;Accession: C;Accession: A;Reference n	nal prot : Romo s 0-Sep-19 on: T147 , R.; He	al procesh DKEZSASHIDAL human (Eregment) Nono sasiem (man) Nono procesh (man) Nono procesh (man) Nono sasiem (man) No	

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1032 LEPCPPRWKVMSLGPCSASCGLGTARRSVACVQLDQGQDVE-VDEAAC-AALVRPEASVP 1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              976 ---ARWQY-KLAACSVSCGRGVVRRILYCARAHGEDDGEEILLDTQCQGLPRPEPQEACS 1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 672 LRPC-ATWHSGNWSKCSRSCGGGSSVRDVQCVDT---RDLRPFHCQPGPAKPPAHRP 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 TMPCTQWVVGPWGQCSAPCGGGVQRRLVXCVNTQTGLPBEDSDQCGH-EAWPESSRPCGT 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALET-CNPQ-PCPARWEVSEPSSCTSAGGAG----LALENETCVPGADGLEAPVTE--- 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 PVPATEPPAAKEEGVIGPWSPSPWPSQAGRSPPPPSEQTPGNPLINFLPEEDTPIGAPDL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 GLPSLSWPRVSTDGLQTPATPESQNDFPVGKDSQSQLPPPWRDRTNEVFKDDEEPKGRGA 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     703 PKPROAMVMAAVRGP---CSVSCCAGLRWWYSCLDOARKELVETVOCGGSGOOPPAWPEA 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVLEPCPPYWAVGDFGPCSASCG-GGLRERPVRCVEAGG-SLLKTLPPARCRAGACQPAV 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSEQPCPARWWAGEWQLCSSSCGPGGLSRRAVICIRSVGLDEQSALEPPACE---HLPRP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 PTETPCNRHVPCPATWAVGNWSQCSVTCGEGTQRRNVLCTNDTGVP-CDEAQQPASEVTC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 SLPLCRWPLGTLGPEGSGSSSHELFNEADFIPHHLAPRPSPASSPKPGTMGNAIEEEA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 PELDLPGPVPVDDFYYDYNFINFHEDLSYGPSEEPDLDLAGTGDRTPPPHSRPAAPSTGS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 PPPVFSWHY----GPWIKCTVICGRGVQRQNVYCLER-QAGPVDEBHCDPLGRPDDQQRK 85
                                                                                                                                                                                                                                                                                                                                                                                                   4.6%, Score 354; DB 2; Length 898;
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tive 65; Mismatches 219; Indels 392;
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962 PGSRREVCQAVPCPARWQ--YKLAACSVSCGRGVVRRILYCARAHGEDDGEEILLDTQCQ 1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 G---PEKGTKFCNIALCPGRAVDGNWNEWS--SWSACSASCSQGRQQRTRECNGPSYGGA 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 ----QTGDPAAREWSPWS-VCSSTCGEGWQTRTRFCVSSSYSTQCSGPLREQRLC---- 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             697 TPTYPQPKPRQAWVWAAVRG---PCSVSCGAG-LRWVNY-SCLDQARKEL-VETVQ---- 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 SWILENPOPERYTLYMKVAKAPVPCS---GPGRVRTYQFDSFLESTRIYLGVESFDEVLR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 LCDPSAPLAFLQASKQFLQMRRQQPPQHDGLRPRAGPPGPTDDFSVEYLVVGNRNPSRAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            781 C------GG-----GLRERPVRCV--EAGGSLLKTLPPAR--CRAGAQOPAVA 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B6 COMICRWIDACLAGSRSSHPCGIMOTPCACLGGBAGGPAAGPLAPRGDVC----LRDAVA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 LETCNPOPC------PARWEV-SEPSSCTSAGGAGLALENETCVPGADGLEAP 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 ---GGPENCLTSLTQDRGGHGATGGWKLWSLWGECTRDCGGGLGTRTRTCLP-----AP 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           865 VIBGPGSVDEKLPAPEPCVGMSCPPGWGHLDATSAGEKA------PSP 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 GVEG-GGCEGVLEEGROONREACGPA-GRISSRSOSLRSTDARRREELGDELQQFGFPAP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      907 WGSIRTGAQAAHVWTPAAGSCSVSCGRGIMELRFLCMDSALRV----PVQEB-LCGLASK 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QOPP----AMPEACVLEPCPPYWAVGDFGPCSAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match Similarity 24.0% Poore 264.5; DB 2; Length 1564; Local Similarity 24.0% Pered No. 11e-06; Length Life 217; Pered No. 11e-06; Concervative 61; Mismatchies 242; Indels 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 217;
                                                                                                                                                                                                                                                                     A.Cross-references: CDB:9838088; OMIM:602682
A.Map position: 8624-8674
C.Superfamily: thromosopondin type I repeat homology
F:469-462/bomain: thrombospondin type I repeat homology <THR3>
A,Status: translated from GB/EWBL/DDBJ
A,Mosicula type: mRA
A,Mosiculas: 1-1184 «MIS
A,Cross-references: EMBL-A&R05297, NID:d1175078; PID:d1024528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      008 DGEBILLDTQCQGLPRP-----EPQEACS-LEPCPPRWKVMSLGPCSASCGLGTARRS 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          060 VACVQIDQGQDVEVDEAACAALVRPEASVPCLIADCTYRWHVG-TWMECS--VSCGDGIQ 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 RRRDICLGPQAQAPVPADFCQHLPKPVTVRGCWAGPCVGQGTPSLVPHEEAAAPGRTTAT 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            627 ORVCOFGIDCGGPNEESQFCYGPPC-AEWIEWCEWSOCSSKCGPGQRIRIRGCLGPNGQE 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                686 -----ATTCQG---PSIBTTLCBGQSCCNWSBWC--HWSM-----CDXBCGGQVRY- 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TEYMPRIGCEWSPCSTQLACEVGVQ 752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 CSCTCGDGAK----SRRRECSTNNCQGADYE---TEPCNLGPCQTWSENCEWSTC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         778 SASCOGGIRERPURCUEAGGSLIKTIPPARCRAGAQQPAVALETCNPQPCP--ARMEVSE 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  515 SASCGSGQRERTRPC-----HLGTNRCEGKDYES----BQCSAGPCPEWSQWE--D 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            836 PSSCTSAGGAGLALENETCVPGADG---LEAPVTEGPGSVDEKLPAPEPCVGMSCPPGWG 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;cross-references: BMBL:268011; PIDN:CAA92014.1; GSPDB:GN00028; CESP:T2186.3
;Experimental source: clone T2186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                () Species: Homo sapiens (man)
C/Date: 2-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 12-Peb-1999
C/Accession: Trools
                                                                                                                          lypochecical procein 12186.3 - Caenorhabditis elegens
C.Species Coenorhabditis elegens
C.Saece 13-00-13-09 sequence_evision 15-00-1999 #text_change 18-Feb-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             718 CSYSCGAGLRWYNYSCLDQARKELVETVQCQGSQQPPAWPEACVLEPCPPYMAVGDFGPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SPW-----QBWS----TCSASCGSGMXR------R
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3.5%; Score 275; DB 2; Length 788; 23.1%; Pred. No. 1.1e-09;

Best Local Similarity 23.18 Matches 112; Conservative

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Query Match

i/Map position: X Ajintrons: 20/1; 47/1; 76/1; 152/1; 735/2; 754/2

Gene: CESP:T21B6.3

i;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-788 <MIL> Submitted to the EMBL Data Library, November 1995 1,Reference number: 219975 1,Accession: T25061

C, Accession: T25061

Mishimond, H.; Skirabunda, T.; Ureno, T.; Kimura, Y.; Kiyono, K.; Tateumi, K.; Yoshisisuhitted to the RMsi Data Library, June 1997 submitted to the RMsi Data Library, June 1997 Spicementon number 241064

brain-specific anglogenesis inhibitor 1 - human NiAlternate names: BAII protein C;Species: Homo sapiens (man)

753 SRSROCVGES-1177 PAGAC 1181 PKPPC 788

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Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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18	867.5	ä	997		ATS7_HUMAN	Ogukp4	nomo
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22	768.5	6.6	930		ATS5 HUMAN	Opuna0	рошо
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SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND DISEASE. STRAIN-DBA/2;

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                                                                                     NGGKYCVGRRMKFKSCNTEPCLKOKRDFRDEQCAHFDGKHFNIN-GLLPNVRM----VPKY
                                                                                                                                                                578 SGILMKDRCKLFCRVAGNTAYYOLRDRVIDGTPC-----GODTNDICVQGLCRQAGCDH
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--- SIMILARITY: Contains I disintegrin-like domain.
-- SIMILARITY: Contains 6 TSP type-1 domains.
-- SIMILARITY: Contains 1 PLAC domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 204-1224 FROM N.A. (ISOFORM 1).
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                                                                                                                                                              MEROPS; M12.026; -. ADAMTS16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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00090; tsp PR01705; TS M00209; TS	ADAM MEPRO; 1. CYSTEINE SWITCH	PS00427; DISINTEGRIN 1,	PSS0214; DISINTEGRIN 2;	PS50900; PLAC;	PS50092; TSP1; 5.	rolase, Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;	, Extracellular matrix,	SIGNAL : 24 POTENTIAL.	P 25 279	CHAIN 280 1224 ADAMIS-16.	DOMAIN 280 495 METALLOPROTEASE.	496 585	586 641	642 746	747 873 SPAC	4 922 TSP	927 987 TSP	988 1048 TSP	1051 1115 TSP	IN 1186 1223 PLAC.	249 249	433 433 ZINC (CATALYTIC)	34 434 BY SIMILARITY.	437 437 ZINC (CATALYTIC) (BY	443 443 ZINC (CATALYTIC) (BY SIM	156 156 N-LINKED (GLCNAC) (310 310 N-LINKED (GLCNAC) (741 741 N-LINKED (GLCNAC) (90 780 N-LINKED (GLCNAC,) (905 905 N-LINKED (GLCNAC) (935	-		VARSPLIC 1073 1224 Missing (In isoform 2).	/FTIG=VSP 007665.	ic dad NT/ W 9 Age TOT TOWNER
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2 Option Propries assessment of the Control of the

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ò	336 VAPGPKAV	CTFAREHLDWCQALSCHTDPLDQSSCSRLLVPLLDGTBCGVEKWCSKGRCR
Q D	520 WQFGEKAKL	LCMLDFKK-DICKALWCHRIGRKCETKFNPAABGTICGHDMWCRGGGCV 575
ò	396 SLVELTPI	SLVELTPIAAVEGRASWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEM 455
Q	576 KYGDEGP-	KYGDEGP-KPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKPCEGSTRTLKL 634
8 1	9 9	PGGAS FYHWG
9	0	3 1
à :	** 1	GESFIMKRODSFLDGTRCMPSGPREDGTLSLCVSGSCRTPGCDGRMDSQQVWDRCQVCGG 573
8	-	₹ ;
ò	574 DNSTCSPR	DNSTCSPRKGSPTA-GRAREYVTFLTTVTPNLTSVYIANHRPLFTHLAVRIGGR 625
g	741 NNSACTIH	RGLYTKHHHTNQYYEMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGH 800
ò	9	
g	801 WTVDWPGR	DYRRSYNEPENLIATGPINETLIVELLFQ 84:
è	4 YGEEY	TREDITFIYEQPKPRQAWWAAVRGPCSVSCGAGLRWVNYSCLD 73:
e e		. 6
à	9	
q	W-DIXEQ-W	MSFCNPXTRPVTGLVPCKVSACPPSWSVGRMSACSRTCGGGAQSRPVQCTRR 957
ò	796 QGSLLKTI	QGSLLKTLPPARCRACAQQPAVALETCNPQPCPARWEVSEPSSCTSAGGAGLALENETCV 855
qq	958 VHYDSEPVPASLC	PASECPQPAPS976
ò	856 PGADGLES	GHLDAT
q	64.6	SRQACNSQSCPPAMSAGPW 995
ò	916 AAHVWTPA	AAHUWTPAAGSCSVSCGRGIMELRFICNDSALRVPVQEELCGLASKPGSRREVCQAV 972
QQ	966	2
ò	973 PCPARP	CPARWQYKLAACSVSCGRGVVRRILYCARAHGEDDGEBILLDTQCQGLPRPE 1025
Q	1046 RCHKPKK	-LASKKCSHLPKPS
ò	1026 POBACSLE	POBACSLEPCPPRWKWNSLGPCSASCGLGTARRSVACVQLDQGQDVEV 1073
e e	1105 LERACAPI	AGPSRGSWFASPWS
ò	1074 DERACRAI	DEAACALVRESSUPC 1090
g	1161 SGCLLP	SGCLLAQYPSASLAC 1175
RESULT TOTAL	### STANDS	STANDAD: PRT, 1593 AA. 4. 41. Created 6. 41. Ans employee width 6. 51. Ans employee 6. 51. Ans employee 6. 51. Ans employee 6. 61. Ans employ

(BY SIMILARITY) (BY SIMILARITY) (BY SIMILARITY)

(POTENTIAL)

POLY-GLU. CYSTEINE SWITCH (ZINC (CATALYTIC)

METAL ACT SITE METAL METAL

DOMAIN DOMAIN DOMAIN DOMAIN

CARBOHYD

1264577; 1264577; 1264577; 1264516 100 invo Chem. 27 1708: Bir 111111.AR Bir 11111.AR Bir 11111.AR Bir 1111.AR Bir	IN: The starty). The precipity of the starty). The precipity of the starty. The precipity of the starty of the starty.	JARITY: UARITY: SS-PROT the Swill pean Bio and this require require an email 250725; JEROOI TEROOI	IPRRODUCE IPRR	Metal Bxtracel 241 241 241 241 241 465 701 701 986 986 986 943
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Pept MICA MIZB. Pept M Zn BS. Peptidase MIZB. Peptidase MIZB. Disintegrin. CAC20419.1; -.

ADAM MEPRO, 1.
CYSTEINE SMITCH, FALSE NEG.
DISINTEGRIN 1; FALSE NEG.
DISINTEGRIN 2; FALSE NEG. propep; 1. 085, TSP 1. ep M12B propep eprolysin; 1. sp 1, 6. TSPIREPEAT.

TSP1, 6. ZINC_PROTEASE, 1. Oprotease, Zinc; Signal; Glycoprotein; Zymogen; BY SIMILARITY. ADAMTS-12. POTENTIAL llar matrix.

METALLOPROTEASE. DISINTEGRIN-LIKE. TSP TYPE-1 1. CYS-RICH. SPACER 1. TSP TYPE-1 2. TSP TYPE-1 3. TSP TYPE-1 4. SPACER 2. TSP TYPE-1 TSP TYPE-1 DOMAIN

LLFQ------VINPGINYEYTIQMGLDNDVZQMYFWQYGHWTECSVTCGTGIRRQTAH 849

92 RORORRANGGILHIELLVAVGPDVFQAH-QEDTERYVLTNINIGAELLRDPSLGAQFRVH 150 Gaps | COTSETTAL
| COTS Query Match

14.5%; Score 1126; DB 1; Length 1593;
Batches 321; Conservative 156; Wismatches 501; Indels 322;
Matches 321; Conservative 156; Wismatches 501; Indels 322; MW; 07F9F48E63BD83A3 CRC64; 10.7 SHELMATTO (19)
2.100 (CATALITO) (19)
2. 1371 1378 1503 177545 M CARBOHYD CARBOHYD CARBOHYD 211 569 386 CARBOHYD CARBOHYD CARBOHYD CARROHYD CARBOHYD SEQUENCE 용 è ag ò

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PTM: The precursor is cleaved by a furin endopeptidase (By

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1086 TSQPILTSQSLSIQPSERNVSSSDTGPTSEGGLVATTTSGSGLSSSRNPITWPVTFFYNT 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     967 SVTCAKNHDEPCDVTRKPNSRALCGLQQCPSSRRVLKPNKGTISNGKNPPTLK-PVPPF 1025
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733 CLDOARKELVETVOCOGSOOPPAMPEACVLEPCPPYWAVGDFGPCSASCG-GGLRERPVR 791
                                                                                                                               350 CIKKGR-GAVKATFCDPETQPNGRQKKCHEKACPPRWWAGEWEACSATCGPHGEKRRTVL 908
                                                                                                                                                                                                                                                  792 CVEAQGSLLKTLPPARCRAGAQQPAVALETCNPQ-PCPARWEVSEPSSCTSAGGAGLALE 850
                                                                                                                                                                                                                                                                                                                                                                                  909 CIQTMVSDEQALPPTDCQ-HLLKPKTLL-SCNRDILCPSDWTVGNWSECSVSCGGGVRIR 966
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10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last sequence update)
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Bickaryota Metacoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrini; Hominidas; Homo.
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QSTEGO;
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Mean 55; Conservative 119; Wismatchee 359; Indels 213; Gaps ene 75;
                                                                                                                                                                                                                                                                                                                                                                                                                   ELG. CONCENTY.

INC. CONCENTY.
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ZINC (CATALYTIC) (BY SIMILARITY)
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                    similarity)
-- SIMILARITY: Belongs to peptidase family M12B.
-- SIMILARITY: Contains 1 disintegrin-like domain.
-- SIMILARITY: Contains 4 TSP type-1 domains.
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DISINTEGRIN-LIKE.
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TSP TYPE-1 3.
TSP TYPE-1 4.
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ADAMTS-18.
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CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ311903; CAC83612.1; -.
Genew; HGNC:17110; ADAMTS18.
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1081 AA;
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dammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo

CBI TaxID=9606;

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975 PARWOYKLAACSVSCGRGVVRRILYCARAHGEDDGEEILLDTOGOGLPRPEPOEACSLEP 1034
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209 PDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPGSGCGPS 268
                                                  397 KNEPCDTLGFAPTSGACSKYRSCTINEDTGLGLAFTIAHESGHNFGMIHDG-EGNFCRA 455
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PRT; 1077 AA.

STANDARD:

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-1- SIMILARITY: Contains 1 disintegrin-like domain.
-1- SIMILARITY: Contains 1 PLAC domain.
-1- SIMILARITY: Contains 5 TSP type-1 domains.
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ADAMTS-10:
METALLOPROTEASE.
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Bukaryota, Metazota, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Buriberia, Rodentia, Sciurognathi, Muridae, Murinae, Mus NCBI_TEATIS_10090; Mus musculus (Mouse)

SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Thymus; MEDLINE=22354683; PubMed=12466851;

Occasaty, Y. Putrucho, M. Rainkawis, T. Adenti, C. Bood R. Kondo, S., Witsadd I., Ossoo M. Saito R., Vitamanka I., Kiyopawa B., Witsadd I., Ossoo M., Saito R., Schondon, C., Ogoloori T., Saiderelli R., Hill Dr., Bill C., Hume D.A., Oscoboubh C., Ogoloori T., Saiderelli R., Hill Dr., Bill C., Hume D.A., Oscoboubh C., Oscobol D., Saito R., Saito S., Saito R., Saito

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SECUENCE FROM N.A.

Gaps Query Match
12.6%; Score 978; DB 1; Length 1213;
gest Local Similarity 27.7%; Pred. No. 2.36-52;
Matches 301; Conservative 133; Mismatches 383; Indels 268;

Sat Mar 13 07:56:20 2004

998 LYCARAHGEDDGERILLDTQCQGLPRPEPQEACSLEPCPPRWKVMSLGPCSASCGLGTAR 1057 .031 ----RNGSDPSKKSYV---VOWLSRPDPDS------PIOXISSKDCCGGD----- 1067 665 426 486 DVQ-HHW----LPHEHRDAKERCHLYCESKETGEVVSMKR--MVHDGTRC----SYKDAF 687 688 ŚLCVRÓDCRKVGCDGVIGSRKQEDKCGVCGGDWIHCKVVKGIFTRSPRKQDYIKMFEIPA 747 658 748 GARHILIOEADITSHHISVKNIETGKFIINEENHIDPNSR--SFIAMGVEWEYR---NED 802 703 853 606 VLEPC-PPYMAVGDFGPCSASCG-GGLRERPVRCVE-AGGSLLKTLPPARCRAGAQQPAV 817 910 NPQECSOPVWVTGEWEPCTQSCGRTGMQVRSVRCIQPLHNNITRSVHTKHCNDHRPE--- 966 877 378 APEPCVGMSCPPGWGHLDATSAGEKAPSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGLME 937 -----RAGS-----WS----QCSVTCGNGTQE 998 PRPQPGSAGHPPDAQ-PGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDFLDQ 367 524 525 YFCKTKKGPPLDGTMCAPGKHCFKGHC---IWLTPDILKRDGNWGAWIPFGSCSRICGIG 581 VKFRTROCDNPHPANGORICSGLAYDFOLCNPODCPNSLADFREEQCOOWD---LYFEHG 638 187 GASFYHWGAAVPHSQGDA--LCRHMC--RAIGESFIMKRGDSFLDGTRCMPSGPREDGTL 542 SLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKG8FT-AGRAREYVTFLTVTP 601 114 VLGMEHDG-QGNRCGDEVRLGSIMAPLVQAAFHRFHWSRCSQQELSRYLHS-----YDC 167 LRDDPFRAHDWPALFQLPGLHYSMNEQCRFDFGLGYMMCTAFRT-FDFCKQLWC-SHPDNP 368 SSCSRLLVPLLDGIECGVERWCSKGRCRSLVELTP-IAAVHGRWSSWGPRSPCSRSCGGG VVIRREQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLEFMSQQCARTDGQPLRSSPG 602 NLTSVYIANHRPLFTHLAVR--IGGRYVVAGKMSISPNTTYPSLLEDG-RVEYRVALTED 659 RIPRIBEIRIMOPIQEDADIQVYRRYGEEYGNLTRPDITFTYF------QP 803 ERETLOTI---GPLHGTITVLVIPE-GD----TRISLTYKYMIHEDSLNVDDNNVLEDD 104 KPRQAMV---WAAVRGPCSVSCGAGLRWWNYSCLDGMRKELVETVGCGGSQQPPAMPEAC 854 AVRHEWALKKWS----PCSKPCGGGGQFTKYGCRRRLDSYMVHRAFCSALAKPKAIRRAC 318 ALETCNPOPCPARWEVSEPSSCTSAGGAGLALENETCVPGADGLEAPVTEGPGSVDEKLP 967 SERACNEELCPGEW 338 LRFLCMDSALRVPVQEELCGLASKPGSRREVCQAVPCPARWQYKLAACSVSCGRGVVRRI 999 RPVLCRIADDNFGVCRE----ERPETAR-ICRLAPCP-----Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Mammalia! Buthekra, Primaces, Catarrhini, Hominidae, Homo. WCRE_TEXTD=6065, Homo sapiens (Human) .058 RSVAC 1062 ADAMTS14. 608 127 . 285 633 543 90 8 윤 a 8 8 용 a ò qq ò q 90 ò a a à CARPERENTAR 8

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MEDINE-2153805; PubMed-11779558.
BOLE M., Remitez A., von Brederlow B., Kubisch C.;
Chizacterization of LAMPHIS4, a movel member of the ADAMTS
metalloprotekinas family."; Biochim. Biophys. Acta 1522:221-225(2001). SEQUENCE FROM N.A. (ISOFORM A) Gene 283:49-62(2002). rissuE=Fetal lung;

Comment=2 isoforms, A (shown here) and B, are produced by use of Event=Alternative splicing, Named isoforms=4; alternative promoters,

Isold=Q8MXS8-3; Sequence=VSP 006958, VSP 005501; Note=Produced by alternative splicing of isoform B;

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— Edward and expression of boxine procellagen; IN-proteiness: a name member of the superfamily of sinc-metalloproteinases with binding stee for calls and other matrix components.
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Gaps Conservative 130; Mismatches 378; Indels 272; 12.3%; Score 955; DB 1; Length 1205; 27.6%; Pred. No. 5.7e-51; Similarity Best Local Sim Matches 297; Query Match

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EVRLGSIMAPLVQAAFHRFHWSRCSQQELSRYLHS-----YDCLRDDPPTHDWPALPQL 24 PGLYYSANBOCRVARGPKAVACTPAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTBC

176 PGLHYSWANDOCHEDPGLGYMMCTAPRT-FDPCKQLWC-SHPDNPYPCKTXKGPPLDGTMC 533 GVEKWCSKGRCRSLVELTP-IAAVHGRWSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAPG 442 APGKHCPKGHC---IWLTPDILKRDGNWGAMSPRGSCSRTCGTGVKFRTRQCDNPHPANG 590 17

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374 -----COSVICGNGIQERPVECRIAD 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    001 DSFGVCREE-----RPETAR-1CRLGPCP-------RN 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 005 GEDDGEEILLDTQCQGLPRPEP----QEACSLEPCPPRWKVMSLGPCSASCGLGTARR-- 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1026 TSDPSKKSYV---VQWLSRPDPNSPVQETSSKGRCQ-----GDKSVFCRMEVLSRYC 1074
GRACVGADLQASMCNTQACEKTQLEFMSQQCARTDGQPLRSSPGGASPYHWGAAVPHSQG 502
                                                                           544 DAKERCHLYCESKETGEVVSMKR--MVHDGTRC----SYKDAFSLCVRGDCRKVGCDGV 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 LAVR--IGGRYVVAGKMSISPNT-TYPSL-----LEDGRVEYRVALTEDRLPRLEEIR 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            568 INGPL------QEDADIQVYRRY-----GEBYGNLTRPDITFTYFQPKPRQAWV 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WAVGDFGFCSASCG-GGLRERPVRCVE-AGGSLLKTLPPARCRAGAQQPAVALETCNPQP 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 WVTGEWEPCSRSCGRTGMQVRSVRCVQPLHNNTTRSVHTKHCNDARPE---GRRACNRBL 968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGSSKQEDKGGVCGGDNSHCKVVKGTFSRBPKKLGYIKMFBIPAGARHLLIOBADTTSHH
                                                                                                                                                                                                                                              DA -- LCRHMC--RAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDSQQVWDRCQVCGGDNSTCSPRKGSPT-AGRAREYVTPLTVTPNLTSVYIANHRPLFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               757 LAVRALETGKFILNEENDVDPNSKTFLAMGVEWEYRDEDGR-----BTLO
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norveqicus (Rat)
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This STATES COVER state is copylight. It is produced through a collaboration between the Bases institute of Bioinformation and the Bouroau collaboration the Barpoau and institutes for finitude. There are no restrictions on its most read and file and file are stated and the state of the stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DOWLNN The spacer chain and the TSP type, identifies are important for a tight interaction with the extracellular matrix.
-FPM: The pecureor is cleaved by a furin endopeptidase (By smillarity).
            --- CONDATTC ANTUNITY Cleaves aggreen at the 1689-101-| iceu-1684
site, within the chondrottin dullate attachent domain.
--- CORFORDER Binds 13th ton probubility (by similarly).
--- STROESLUAR JOCATION: Secreted. Associated with the extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               matrix (By similarity).
-!- INDUCTION: Down-regulated in endothelial cells derived from
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PROGETE; PSQ124; INTENDERINE, PROGES, PSQ124;
PROGETE; PSQ124; PSQ124;
PROGETE; PSQ124; PSQ12
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ZINC (CATALYTIC) (BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i-SIMILARITY: Belongs to peptidase family M12B.
-i-SIMILARITY: Contains 1 distincegin.—ilke domain.
-i-SIMILARITY: Contains 3 75P type-1 domains.
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METALLOPROTEASE.
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SPACER.
TSP TYPE-1 2.
TSP TYPE-1 3.
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STRAINESprage-loakley, TISSUR-Brain, List X. To Y. Y. Yin T. Youngarene E.M., Stephanson D.T., Clemens J.A., Little S.J., Y. Yin T., Volumetrne E.M., Stephanson D.T., Clemens J.A., Tinducis on a distincent and mesalloprocesses with the thrombospoint hype I made (I (DAMPS) a Submitted (DAWY-1999) to the SPBU/Comban/JODBA databases.

SEQUENCE FROM N.A. NCBI_TaxID=10116;

us-09-836-712-2.rsp

---GECSKTCGSG--W------QRRVVEC 881 PPYWAVGDFGPCSASCGGGLRERPVRCVEAQG 797 C-PRWQVGDWSPCSKTCGKGYKKRTLKCLSHDG 940 tr., Stormer C.M., Schuler C.D., Schuler C.M., Index C.M., Index C.M., Index C.M., Index C.M., Index C.M., Schuler C.D., Schwer T.E., Schwer T.M., Schuler C.M., Schwer S.M., Schw g a new type of metalloproteinase-mbospondin motifs as an update)
in update)
disintegrin and metalloproteinase
TS 1) (ADAM-TS1). ima K.; romosomal mapping of the mouse y protein with TSP motifs."; ta, Vertebrata, Euteleostomi, gnathi; Muridae, Murinae, Mus ; nase associated with the jiki F., Ichimura F., 99-16903 (2002) . LKKPKHY 957 PCPARW 831 GLU-403. 968 AA

us-09-836-712-2.rsp

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FÜNCTION, AND INDUCTION.
MEDLINES-20241357; PLANSGES10781075;
ROKNET R.L., Russell D.L., Espoy L.L., Lydon J.P., O'Malley B.W.,
Richards J.S.)
MEDLINE-20189568; Pubbled-10930576;
Kino K., Okada Y., Kavatijaa H., Nakamura H., Niyasaka M.,
Okno H., Matsuthina K.,
Miburkal Jahawsa a certilage proteoglycan, aggrecan.";
FEBS Lett., 478:241-245(2000)
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ZINC (CONDAINT) (SE SERLIABELY)
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CYSTEINE SWITCH (POTENTIAL). ZINC (CATALYTIC) (BY SIMILARITY)

ACT SITE METAL XETAL CARBOHYD CARBOHYD CONFLICT PARBOHYD ARBOHYD STAGEN

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METALLOPROTEASE. DISINTEGRIN-LIKE. TSP TYPE-1 1. CYS-RICH. SPACER. TSP TYPE-1 S. TSP TYPE-1 3. POLY-ARG.

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POTENTIAL ADAMTS-1

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SINGLINIAR LOCATION: Secreted. Associated with the extraoellular | BORGA | BORG INDUCTION: Induced in vitro in colon adenocarcinoma cells by interleukin-1, or in vivo in kidney and heart by lipopolysaccharide. Also induced by IM stimulation in granulosa cells of preovularcry follicies. or send an email to license@isb-sib.ch)

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-!- DOMAIN: The spacer domain and the TSP type-1 domains are important	for a tight interaction with the extracellular matrix.	-i- SIMILARITY: Belongs to Debtidase family MI28.	-!- SIMILARITY: Contains 1 disintegrin-like domain.	!- SIMILARITY: Contains 3 TSP type-1 domains.	-1- CAUTION: Ref. 2 sequence differs from that shown due to a	frameshift in position 7.		This SWISS-PROT entry is copyright. It is produced through a collaboration	etween the Swiss Institute of Bioinformatics and the EMBL outstation -	he European Bioinformatics Institute. There are no restrictions on its	se by non-profit institutions as long as its content is in no way	modified and this statement is not removed. Usage by and for commercial	ntities requires a license acreement (See http://www.isb-sib.ch/announce/
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. Max 13 07:56:20 2004 u.	711NAVNEDPGNS-GAGLARONS-CLIDANZELVETUCO. 82 ERI	AND SHOWN STANDED: PRF. 1211 AA. SASS. SAS	Discrementally by the presents in skin of procolleg processed at the N-terminus SIMILARITY: Belongs to peptidase family M12B SIMILARITY: Contains I disintegrin-like domain.
Sat	868686	는 함은 8 % 1 개인 전 1 등 1 대로 하면 없었다. 다른 1 대	

This SARS-STORT marty is copyright. It is produced through a collaboration between the Sales Institute of Michiganian produced that the Brogan collisional mixture of the same are no restrictions on its the Brogan collisional mixture. There are no restrictions on its the Brogan collisional mixture are no restrictions on its the area of the same are not set of the same and the same area of the same area of the same and the commercial mixture as itemate as the same agreement (see http://www.isb-sib.ci.anzounce) or send an easil to licensesial-sib.ci). PRPGAVAHACYPST | March | Marc BY SHILDSTY.

ZINC (CARALITC) (BY SHILLSTY).

ZINC (CARALITC) (BY SHILLSTY).

LINKED (CARAC).

LINKED (CARAC TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
BLAC.
POLY-ALA.
DOLY-GLD.
ZINC (GRALATIC) (BY SINILARITY). HCFKGHCIWLTDILKRDGSWGA -> F: LGGGGRWIA (in isoform SpNPI) /FIId=VSP 005497. Missing (in isoform SpNFI). /FTId=VSP 005498. MW; BECEEF25C23CAD2D CRC64; -i- SIMILARITY: Contains 1 FLAC domain.
-i- SIMILARITY: Contains 4 TSP type-1 domains.
-i- CAUTION: Has sometimes been referred to as ADAMTS3. EMBL, AJ003125; CAA05880.1; ... MEROPS, ML2.301, ... 1211 AA, 134722 Senew; HGNC:218; ADANTS2. 971 1029 1097 ACT SITE METAL METAL CARBOHYD CARBOHYD CARBOHYD CARBOHYD TARBOHYD /ARSPLIC ARSPLIC SEQUENCE PARBOHYD

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DNA Res. 7:65-73 (2000).
                                                                                                 Homo sapiens (Human)
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                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                              FISSUE-Heart;
974 LCPGRWRAGPWSQCSVTCGNGTQERPVPCRTADDSP-----GICQEBRPETARTCRL 1025
                                 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               026 GPCP-----RNISDPSKKSYVVQMLSRPDPDSPIRKISSKGH----CQGDKSIFC---- 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209
                                                                   149
                                                                                                                                SO HLVKNVILTEPEGAPNI-TANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLEL 208
                                                                                                                                                    114 VLVRIILLSYGKSMSLIEIGNPSOSLENVCRWAYLQQKPDTGHDEYHDHAIFLTRQDF-- 371
                                                                                                                                                                                                209 PDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAMEIGHSFGLEHDGAFGSGGGFS 268
                                                                                                                                                                                                                                                                ---GHVMASDGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWD-----PPRPQPGSAGH 318
                                                                                                                                                                                                                                                                                                                                                              ----LPGLHYSMNEOCRPDFGLGYMCTAFRT-PDPCKQLMC-SHPDNPYFCKTKKGPPL 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCDGVIGSSKOEDKCGVCGCDNSHCKVVKGTFTBSPKKHGYIKMFEIPAGARHLLIOBVD 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             613 PLFTHLAVR--IGGRYVV-----AGKMSISPNTTYPSLLEDGRVEYRVALTEDRLPR 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               804 -ETLQTMGPLHGTITVLVI----PVGD-TRVSLTYKYMIHEDSLNVDDNNVLEEDSVVY 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             710 VWAAVR-GPCSVSCGAGLRWVNYSCLDQARKELVETVQCQGSQQPPAWPEACVLEPC-PP 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               857 EWALKKWSPCSKPCGGGGSQFTKYGCRRRLDHKKVHRGFCAALSKPKAIRRACNPQECSQP 916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               917 VWVTGEWEPCSQTCGRTGMQVRSVRCIQPLHDNTTRSVHAKHCNDARPE---SRRACSRE 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             926 PCPARWEVSEPSSCTSAGGAGLALENETCVPGADGLEAPVTEGPGSVDEKLP-APEPCVG 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             985 MSCPPGWGHLDATSAGEKA------PSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGLM 936
                                                                                                                                                                                                                              --GPSGMGGYAPVTGMCHPVRSCTLNHEDGFSSAFVVAHETGHVLGMEHDG-QGNRCGDE 428
                                                                                                                                                                                                                                                                                                                                319 PPDAQPGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLL 378
                                                                                                                                                                                                                                                                                                                                                                                                DGTECGVERWCSKGRCRSLVELTP-IAAVHGRWSSWGPRSPCSRSCGGGVVTRRROCNNP 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 RPAFGGRACVGADLQAEMCNTQACEKTQLEFMSQQCARTDGQPLRSSPGGASFYHWGAAV 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHSQGDA--LCRHMC--RAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTF 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              645 PHEHRDAKERCHLYCESRETGEVVSMKR--MVHDGTRC----SYKDAFSLCVRGDCRKV 697
                                                                                                                                                                                                                                                                                              429 VRLGSIMAPLVQAAFHRFHWSRCSQQELSRYLHS--YDCLLDDPFAHDWPALPQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                    DGTMCAPGKGCFKGHC---IWLTPDILKRDGSWGANSPFGSCSRTGGTGVKFRTRQCDNP
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                                                                91 QRQRQRRAAGGILHLELLVAVGPDVFQAH-QEDTERYVLTNLNIGAELLRDPSLGAQFRV
                                                                                                 254 RRRARRHAADDDYNIEVLLGVDDSVVOFHGKEHVOKYLLTLMNIVNEIYHDESLGAHINV
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                                 276; Conservative 119; Mismatches 390; Indels 150;
12.1%; Score 941; DB 1; Length 1211; 29.5%; Pred. No. 4.2e-50;
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ATS1 HUMAN STANDARD; PRT; 967 AA. Q9UHI8; Q9NSJ8; Q9PZKO; Q9UH83; Q9UP80;

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Segionne general R. Panked-10830551, Recurble H. Pand Toper Y. A. Panded-10830551, Recurble H. Pand Toper Y. A. Panced H. Pand Toper Y. A. Panced H. Panded H. Panded H. Panded H. Groner Y. A. Banded H. Panded H. Pand
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Lombardo M., Irusha-Arigow M., Welli-A., Mand WETH-2 are members of a new
Yesth-1. a Thream ortholog of ADAMTS-1, and METH-2 are members of a new
family of processing with angol-finiblicory activity.";
7.3 sloid. Chem. 774:53449-535971899).
90-08Y-2000 (Sen. 35, Creates)
16-OFT-2001 (Sen. 46, Lame sequence update)
10-OFT-2001 (Sen. 46, Lame annotestou update)
ADAMYS-1 precursor (EG 3.4.24.-) (A dishinegrin and mecalloproteinase
with birarcopposidin nocif. (EG 3.4.24.-) (A dishinegrin and mecalloproteinase
ADAMYS-1 GW NERHI OW KIXALIA66.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Oliench G. Schmitt D. K. O., Fillareky C., Hinzmann B., Weise B.,
Rosenthal A., Threatuch K., Hareky C., Hinzmann B., Meise B.,
Dolfferential gene expression by endothelial cells in distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gasas C., Pritchard M.A., Estivill X., Arbones M.L.;
"Cloning, characterization and mapping on human chromosome 21
orthologue of murine Adamts-1.";
Submitted (Uni-1999) to the EMBL/GenBank/DDBJ databases.
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Eur. J. Biochem. 267:2820-2830(2000).
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MEDLINE=20181126; PubMed=10718198;
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us-09-836-712-2.rsp

Length 967

11.8%, Score 914;

105383 MW; C189389324741ED1 CRC64; DB 1,

967 AA;

SQ SEQUENCE Query Match

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EMEL, AFTONOS, AMESTIZ.1.

EMEL, AFONOS, AMESTIZ.1.

EMEL, AFONOS, AMESTIZ.1.

EMEL, ARONTST, IMAGESS, 1.1

EMERSOES, IMAGESS, 1.2

GREGOS, 1.2

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ADANTS-1.
BY SIMILARITY.
DISTALEGRIN-LIKE.
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CYS-RICH.
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Best Loc Matches	238, 83 E	Best Local Similarity 28.7%; Pred. No. 1.5e-69. Macches 238, Conservative All Mismatches 319, Indels 134, Gaps 31, Masches 238, Masches 210, Mismatches 319, Indels 134, Gaps 31, Masches 238, Masches 210, Mismatches 319, Mi
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> 0	136 E	ELLADPSLGAQFRVHLVRAVLLTBEBGARNITANLTSSLLSVCGWSQTINPEDDTDPGHA. 195 ALYGHGSTRSSVSLVVVTLIVHEDBORBETTSNALTENFCXMOXGMIPPSRAAT 350
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1321 NAGGCRLFINVAPHARIAIHALAINMGAGTEGANASYILIRDTHSLRTTAFHGQQVLYNE 1380
961 ACSVSCGRGVVRRILYCARAHGEDDGEBILLDTQCQGLPRPEPQEACSLEPCPPRWKVMS 1020
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                                      LGPCSASCGLGTARRSVACVQLDQGQDVEVDBAACAALVRPEASVPCLIADCTVRWHVGT
                                                                       1021 LGPCSASCGLGTARRSVACVQLDQGQDVEVDBAACAALVRPBASVPCLIADCTYRWHVGT
                                                                                                                  1104 WMECSVSCGDGIQRRRDTCLGPQAQAPVPADFCQHLPKPVTVRGCWAGPCVGQGTPSLVP
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                                                                                                                                                                                                      1164 HEBAAAPGRITATPAG-----ACGROHLEPI
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                                                                                                                                                                                                                                                                                  GTIDNRGPGQADCAVAIGRPLGEVVTLRVLESSLNCSAGDMLLLWGRLTWRKOMCRKLLDM
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                                                                                                                                                                                                                                                                                                                                                                                                         261 TPSSKINTLVVRORCGRPGGGVLLRYGSQLAPETFYRECDMQLFGPWGEIVSPSLSPATS
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three snowl genes in human chronosees 934,". I
Submitted (889-199) to the PREL/GenBank/Orbil database.
BERL, MOILTM, CASSIST, 1; FEP. "IncerPool 18800884, TSP.". IncerPool 18800884, TSP.". IncerPool 18800884, TSP.".
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Mammalie, Butheria, Primates, Catarthini, Hominidae, Homo.
NCDI_TAXLD-9606;
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Young J.M., Woodward K.J., Aziz S., Burley M., Kwiatkowski
Povey S.N.
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Last annotation update)
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Pred. No. 1.38-124;
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SMART) SM01005; TSP1, TSP1, SM0209; TSP1, 1. Hypotherical protein.
SEQUENCE 364 AA; 3864 MM;
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01-MAY-2000 (TrEMBLrel.
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                                                                                                                                               24 NHORHPRARCPPLCVAGILACGFLLGCWGPSHFQQSCLQALEPQAVSSYLSFGAPLKGRP
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VON WILLEBRAND FACTOR-CLEAVING PROTEASE
                                                               Length 1427;
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    75 1427 VON MILLEBRAND FACTOR-CLEAN.
1427 AA; 153632 NN; EBIBC3AABC1A4442 CRC64;
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Matches 1392;
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90 RORORORRAAGGILHLELLVAVGPDVFQAH-OEDTERYVLTNINIGAELLRDPSLGAOFR 148 237 KSKSLSRRSISKERWVETLVVADIKTVEYHGSENVESYILTIMOMVIGLFHSPSIGNLVH 296 149 VHLVKAVILTEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDFGHADLVLYITRFDLEL 208 297 IVVVRLILLEEBERGGLKIVHHABKTLSSFCKWQKSINPKSDLNPVHHDVAVLITRKDI-C 355 209 PDGNR--QVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPGSGCG 266 356 AGVNRPCETLGLSQLSGMCQPHRSCNINEDSGLPLAPTIAHELGHSFGIQHDGKE-NDCE 414 267 PSG---HVMASDGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQPGSAGHPPDAQ 323 115 PVGRHPYIMSQOIQYDPTPLTMSKCSKEYITRFLDRGRGFCLDDIPSKKGLKSN---VIA 471 324 PGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC '383 472 PGVIÝDVHHOCOLOYGPNA---TFCOEVENVOOTLWCSV----KGFČRSKLDAAADGTRC 524 384 GVEXMCSKGRCRSLVELTPIAAVHGRMSSWGPRSPCSRSGGGGVVTRRRQCNNPRPAFGG 443 525 GEKXWCMAGKCIT-VGKKP-ESIPGGKGRWSPWSHCSRTCGAGAGSAERLCNNPEPKFGG 582 444 RACVGADLQAEMCNTQACEKTQLEFMSQQCARTDGQPLRSSPGGASFYHW----GAAVPH 499 583 KYCTGERKRYRLCNVHPCRSDTPTFRQMQCSEFDTVPYKN----QFYRWFPVFNAAHF- 636 500 SQGDALCRHWCRAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRM 559 637 -----CELYCRPIDEQFSERMLEAVIDGTPCFEGG----NSRNVCINGICKRVGCDYEI 686 560 DSQQVWDRCQVCGGDNSTCSPRKGSFTAGRARRYVTFLTVTPNLTSVYIANHRPLFTHLA 619 Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Kammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mur XCSI_TAXID=10099; Cuery Watch
14.74; Score 1138.5; DB 11; Length 1600
Bet Local Similarity 25.54; Pered. No. 6-75;
Matches 33; Conservative 15; Wismatches 503; Indels 327; Cal S., Lopez-Ctin C., "Mouse JADMYS-12." "Submitted (JAN-2003) to the ENBL/GenBank/DDBJ databases. ENBL, NESST422; Oxf0596. 1600 AA; 177791 MW; 083089D356E38C5D CRC64; Mus musculus (Mouse) Integrin, Protease. SEQUENCE 1600 AA; SEQUENCE FROM N.A. SO WHEN THE PROPERTY OF THE PR 유 à Š 유 à ò g à 1254 KTNTLVVRORCGRPGGGVLLRYGSQLAPETFYRECDMQLFGPWGEIVSPSLSPATSNAGG 1313 1314 CRLFINVAPHARIAIHALATNMGAGTEGANASYILIRDTHSLRTTAFHGQQVLYWESESS 1373 120 180 591 240 EYVTFLTVTPNTSVYIANHRPLFTHLAVRIGGRYVVAGXMSISPNTTYPSLLEDGRVEY 300 EYVIPLIVIPNLISVYIANHRPLFTHLAVRIGGRYVVAGXMSISPNTTYPSLLEDGRVEY 651 9 1194 MRGPGQADCAVAIGRPLGEVVTLRVLESSLNCSAGDMLLLWGRLTWRKMCRKLLDWTFSS QCARTDGQPLRSSPGGASFYHWGAAVPHSQGDALCRHMCRAIGESFIMKRGDSFLDGTRC OCARTDGQPLRSSPGGASFYFWGAAVPHSQGDALCRHMCRAIGESFIMKRGDSPLDGTRC MPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAR 181 MPSGPREDGTLSLCVSGSCRIFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAR 1 MRGPGQADCAVAIGRPLGEVVTLRVLESSLNCSAGDMLLLWGRLTWRKMCRKLLDMTPSS 61 KTNTLVVRORCGRPGGGVLLRYGSGLAPETFYRBCDMOLFGPWGEIVSPSLSPATSNAGG 121 CRLFINVAPHARIAIHALATNMGAGTEGANASYILIRDTHSLRTTAFHGOOVLYWESESS 0; Gaba Bikaryota, Metazoa; Chordata; Craniata; Vertebrata; Direleostomi; Mammaila, Butheria; Primates; Catarrhini; Rominidae; Homo. NCBL_EATD=9606; Without State of the American Process of the American State of the Query Match 15.3%; Score 1185; DB 4; Length 223; Best Local Similarity 100.0%; Pred. No. 1.64-79. Matches 223; Conservative 0; Mismatches 0; Indels (Matches 223; Conservative 0; Mismatches D; Indels (Matches 223; Conservative 0; Mismatches D) 1374 QAEMEPSEGFLKAQASLRGQYWTLQSWVPEMQDPQSWKGKEGT 1416 QAEMEFSEGFLIKAQASLRGQYWTLQSWVPEMQDPQSWKGKEGT 223 Hypothetical protein. SEQUENCE 223 AA: 24546 MM; 928EFDDD77088D28 CRC64; 01-WAR-2001 (TRMBLER]. 16, Created)
01-WAR-2001 (TRMBLER]. 16, Last sequence update)
10-07-2003 (TRMBLER]. 25, Last amocation update)
1Mpochesical protein. 223 AA 552 RVALTEDRIBERRINGPLOEDADIQV 680 RVALTEDRIPRIERIRIWGPLOEDADIOV 329 PRELIMINARY; PRELIMINARY; Homo sapiens (Human). SECUENCE FROM N.A. TISSUE-Testis Q9H0G3 Q9H0G3; Q811B3 Q811B3, RESULT 4 RESULT 3 0611B3

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Gaps

DB 11, Length 1600;

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          [2]
SEQUENCE PROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 PFYSTMTTDPEVEIHSGSGEDSDQPLNKDKSNSVIWNKIGVPEHDAPMETDAELFLGFPF 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 TSYMGEEPSWPPFSTXMEGSLPAWSFXNETRIDGMI--AEKSRKIPLPLAGDHHPATSE 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1367 KLENHDKLALPNITNPTQGFGPVLTEEDASNLIAEGFILMASDYKHLMKDHSPAYWIVGN 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       982 LAACSVSCGRGVVRRILYCARAHGEDDGEEIILDTQCQGLPRPEFQBACSLEPCPPRWKY 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1327 WSKCSTTCGLGAYWRSVECSSG------VDADCTTIORPDPAKKCHLRPC-AGWRV 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1042 MSLGPCSASCGI/GTARRSVACV-OLDOGODVEVDEAACAALVRPEASVPCLIADCTYRWH 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 GNWSKCSRNCSGGFKIREVQCMDSLDHHRSLRPFHCQFLAGAPPLSMSCNLEPCG-EWQ 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  969 RIRSVÍCAKOMINEPCDKTRKPNSRALGGLÓGCPFSRRULKPHKDIAÞSGKNOSTAEHDPF 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .029 KPIPAPISRPTPLSIPTVPESMSTSTPTINSLGSTIASQEDANGAGWONNSTQAEEGSHP 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             866
                                                                                                                                                                                                                              747 IRSEDPEKYYLNGGFILGWNGNYK--LAGTVPQY-----DRKGDLEKLIAPGPINESVW 798
                                                                                                                                                                                                                                                                                                                                                       729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- EGPGSVDEKLP-APEP 881
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DSNATEDROGVCLGDGSACQTVKKLFRQXEGSGYVDIGLIPKGARDIRVMEIKAAGNFLA 746
                                                                                                                                                       VRIGG--RYVVAGKOMSISPNTTYPSLLEDGRVEYRVALTEDRLPRLEEIRIWGPLQEDAD 677
                                                                                                                                                                                                                                                                                                                                                                                                          99 LOLLPO------VINPGIXYEYTVRXDGLDNDVBKLLYFWQFGRWIECSVICGIGIRRQ 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  852 AAHCVKKGH-GIVKTIPCNPEIQPSVRQKKCHEKDCPPRWWAGEWEACSTICGPYGEKKR 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1101 VGTWMECSVSCGDGIQRRRDTCLGPQAQAPVPADFCQHLPKPVTVRGC-----WA 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1435 VEPMSQCSRSCGGGVQERGVSC------PGGLCDWTKRPATTVPCNRHLCCHWA 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             789 PVRCVEACGSLLKTLPPARCRAGACOPAVALETCNPO-PCPARWEVSEPSSCTSAGGAGL
                                                                                                                                                                                                                                                                                                                                                       IQVYRRYGEEYGNLTRPDITFTYPQPK-----PRQAWWAAVR-GPCSVSCGAGLRWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYSCLDOARKELVETVOCOGSOOPPAMPEACVLEPCPPYWAVGDFGPCSASCGG-GLRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----BAPVT
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118 PCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLOAEMCNTQACEKTQLEFMSQGCARTD 477 178 GOPLRSSPGGASFYHWGAAVPHSOGDALCRHMCRAIGESFIMKRGDSFLDGTRCMPSGPR 537 91 ORORORRAAGGILH-LELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQPRV 149 ----SGHVMASDGAAPRAGLAWSPCSRROLLSLL--SAGRARCV 305 162 TDPLDQSSCSRLLVPLLDGTECGVEK--WCSKGRCRSLVELTP--IAAVHGRWSSWGPRS 417 TFYGSOMGCRIQHMPWADGTPCDESRSMPCHHGAC----VRLAPESLIKIDGQWGDWRSWG 613 114 ECSRICGGGVOKGLRDCDSPKPRNGGKYCVGQRERYRSCNTQECPMDTQPYREVQCSEFN 673 267 REARSHRAANSWOHYVEVLVVADTRAYEYHGRSLEDYVLTLFSTVASIYRHOSLRASINV 326 150 HIVKAVILTEPEGAPNITANLISSLLSVÇGWSÇTINPEDDIDEGAADLVLYITRFDLELP 209 327 VVVKLIVLKTENAGPRITQNAQQTLQDPCRWQQYYNDPDDSSVQHHDVAILLTRKDICRS 386 210 DGNRQVRGVTQLGGACSPTWSCLITEDIGFDLGVTIAHEIGHSFGLEHDGAPGSGCGP-- 267 387 OGKCDTLGLAELGTMCDMOKSCAIIEDNGLSAAFTIAHELGHVFSIPHDDE--RKCSTYM 444 4.45 PVNKVCKFQSTKFDKTQFQNNFHIMAPTLEYNTHPWSWSPCSAGMLERFLENNRGQTQCL 504 106 WDPPRPOPGSAGHPPDA----OPGLYYSANROCRVAFGPKAVACTFAREHLDMCQALSCH 361 Gabs Best Local Similarity 26.6%; Fred. No. 2.305.73; Matches 331; Conservative 142; Mismatches 501; Indels 272; / March 14.4%; Score 1118; DB 5; Length 2165; Local Similarity 26.6%; Pred; No. 2.96-73;

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Caenorhabdítus elegans. Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabdítida, Rhabdítoidea,

Rhabditidae, Peloderinae, Caenorhabditis NCBI_TaxID=6239;

01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-COT-2003 (TrEMBLrel. 25, Last annotation update)

725H8.3 protein. Q19791 PREJ Q19791, Q27524;

F25H8.3

PRELIMINARY;

Gajadaty S.; Submitted (FEB-1996) to the RMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

574 NKDIGIOGVASTNIHWYPKYANVAPNERCKLYCRISGSAAFYLLRDKUVDGTPCDRNGD- 732

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1015 IDCSGRKWNYGEWTSCSETCGSNGRMRKSYCVDDSNRRVDESL-C-GREGKEATERECN 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1073 RIPC-PRWVYGHWSECSRSCDGGVKMRHAQCLDAADRETHT---SRC-----GPAGTQEH 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1124 CNEHAC-TWWQFGVWSDCSAKCGDGVQYRDANC---TDRHRSVLPEHRCLKOMEKI-ITKP 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CMDSALRVPVQEELCGLASKPGSRREVCQAVPCPARWQYKLAACSVSCGRGVVRRILYCA 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CV-SGNGTEVDMSLCGTASDRPASHQTCNLGTCPFWRNTDWSACSVSCGIGHRERTTECI 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVQLDQQQDVEVDEAACAALVRPEASVPC-----LIADC-TYRNHVGTWMEC 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTRGSEG--TIVDEYFCDRNTRPRLKKTCEKDTCDGPRVLQKLQADVPPIRMATGPWTAC 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            956 IDCSTRWITEDV-SSCSAKCGSGQKRQRVSCVKMEGDRQTPASEHLCDRNSKPSDIASCY 1014
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                                         733 -----DICVAGACMPAGCDHQLHSTLRRDKCGVCGGDDSSCKVVKGTFNBQGTFGYNEVM 787
                                                                                                                 651
                                                                                                                                                                 788 KIPAGSANIDIRQKGYNNMKEDDNYLSLRAANGBFLLNGHROVS-LARQQIAFQDTVLEY 846
                                                                                                                                                                                                                             RVALTEDRIBERRERIRIWGPLQEDADIQVYRRYGERYGNLTRPDITFTY-----FQ 702
                                                                                                                                                                                                                                                                                                                                                                                                           896 PISSALYLWRVIDIWIECDRACRGQQQQQKLMCLDMGIHRQSHDRNCQNVLKPKQATRACN 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNPOPCPARWEVSEPSSCTSAGGAGLALENETCVPGADGLEAPVTEGPGSVDEKLPAPEP 881
EDGTLSLCVSGSCRIFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRARBYVTFL 597
                                                                                                                                                                                                                                                                                         S---GSDAI--IERINGTGPIRSDIYUHVL----SVGS-HPPDISYEYMTAAVPNAVIR 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 -----wumanargpcsvscgaglr-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----WWYS------CLDQARKELVETVQCQGSQQPPAWPEACV
                                                                                                           TVTPNLTSVYIA-----NHRPLFTHLAVR-IGGRYVVAGKMSISPNTTYPSLLEDGRVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    762 LEPCPPYWAVGDFGPCSASCGGGLRERPVRCVEAGGSLLKTLPPARCRAGAGGPAVALET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVGMSCPPGWGHLDATSAGEKAPSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGLMELRFL
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Elikaryota, Metacoa; Chordata; Craniata; Verebrata; Buteleostomi;
Mammalia; Buthenia; Rodentia; Schurognathi; Muridae; Murinae; Mus
NCBI_BAZD-1090;
                                                                                                                                                                                    [1]
SERVINCE FROM N. A.
STRAIN-COTHEL, J. TESSUE-Dre,
THE PROTON COMPOSET, P. DRAMGALIGAGESI,
THE RIVING COMPOSET STRAIGHT Research Group Phase I & II Team;
                                                     Vikh2:001 (TEMBRILE). 2. Created

0:-MAX-2001 (TEMBRILE). 2), Last sequence update)

0:-MAX-2001 (TEMBRILE). 2), Last amotation update)

Mypotherical metalloprotease.

Mis musculus (Mouse).
RESULT 6
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The "Amalysis of the mouse transcriptome based on functional annotation of Manalysis of CALL. Replace CALL. Assertion of Manalysis of CALL. Assertion of Manales CALL. Assertion of Manales CALL. Assertion of Manales CALL. Assertion of CALL. Assertion of Manales CALL. Assertion of CALL. Assertion of

Query Match 14.4*; Score 1116.5; DB 11; Length 1092; Bast Local Similarity 28.7*, Pred. No. 1.5e-7. Indels 235; Gaps Mismatches 292, Indels 235; Gaps

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94 RORRANG---GILHLELLVAVGPDVPQAH-QEDTERYVLTNINIGAELLRDPSLGAQFRV 149 109 RPRRSAGKSQNGLNVETLVVADAKNVEKHGKDDVTTYILTVNRMVSSLFKDGTIGSDINI 168 150 HLVKMVIL-TEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDFGHADLVLYITRFDL-E 207 WANEPODILGFADISGMCSKYRSCIINEDTGLGIAFITAHBSGHNFOMVHDG-EGNPCRK 283 268 S-GHVMASDGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQPGSAGHPPDAQPGL 326 284 ABGNIMSPTLIGNNGVFSWSSCSRQYLKKFLSTPQAGCLVDEPK-QTGQYKY-PDKLPGQ 341 169 VVVSIILLEBEPPEGL-LINHHADGSLNSFCQMQSALVGKNRHDHA---ILLTGFDICS 108 LPDGNRQVRGVTQLGGACSPTWSCLITEDTGRDLGVTIAHEIGHSFGLEHDGAPGSGCGP ò

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ò 8 507 RHMCRAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWD 566 567 ROQVOGGDNSTCSPRKGSF-TAGRARBYVTFLTVTPNLTSVYIANHRPLFTHLAVR-IGG 624 565 ACGUCKGDNSTCKFYKGLYLSQHKANBYYPVVTIPAGARSIBIQBLQLSSSYLAVRSLSQ 624 511 KLYCKARNFEFFRAMSGKVKDGTPCSPH--RND----VCIDGICELVGCDHELGSKAVSD ò 8 ò

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637 -----CELYCRPIDEQFSERMLEAVIDGTPCFEGG----NSRNVCINGICKRVGCDYEI 686
                                                              560 DSQQVWDRCQVCGGDNSTCSPRKGSPTAGRARBYVTFLTVTPNLTSVYIANHRPLFTHLA 619
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PROSITE, PS00142; ZINC PROTEBSE: 1.
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the First Concern Exploration Research Group Phase I & II Team;

the First Concern Exploration Research Group Phase I & II Team;

the First Concern Exploration Research Group Phase I & II Team;

the First Concern Exploration Research Group Phase I & II Team;

the First Concern Exploration Research Group Phase I & III Team;

the First Concern Exploration Research Research Exploration Research Research Research Research Research Research Research Research Research Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 PDGNR -- QVRGVTQLGGACSPTWSCLITEDIGFDLGVTLAHEIGHSFGLEHDGAPGSGCG 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 RSRSLSRRSISKERWVETLVVADTKTVBYHGSENVESYILTIMAMVTGLFHSPSIGMLVH
                                                                                                                                                                Sakkaryota; Metanga; Chondata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodenta: Sciurognathi; Muridae; Murinae; Mus
NGB_TRAIL=10000;
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11.14; Score 1013.5; DB 11; Length 1009; Best Local Similarity 31.81; Pred; No. 5:06-66; Mest Local Similarity 11; Mismatches 361; Indels 75; (Matches 261; Indels 75; (Matches 261; Indels 75; (Matches 261); Indels 
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
ADAMTS-12 precursor (Fragment).
A1605170.
                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                           SEQUENCE PROM N.A.
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620 VRIGG--RYVVAGNOSISPNTTYPSLLEDGRVEYRVALTEDRLPRLEEIRIMGPLQEDAD 677
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                                                                                                                                                                                                                                                                                                                                                                                                                      678 IQVYRRYGBEYGNLTRPDITFTYFQPK-----PRQAWVWAAVR-GPCSVSCGAGLRWV 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 LÖLLFQ------VTNPGIKYEYTVRKDGLDNDVEKLLYFWQFGRWTECSVTCGTGIRRQ 851
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687 DSNATEDRÇGÝCLGDGSACQTVKKLFRQKEGSGYVDIGLIPKGARDIRVMEIKAAGNFLA 746
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12.0%, Score 933, 198 6; Length 759,
set Local Similarity 30,0%; Pred, No. 3.58-60,
Notches 2.40; Conservative 111; Mismatches 327; Indels 122;
Notches 2.40; Conservative 111; Mismatches 327; Indels 122;
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01-MAR-2003 (TERMELTEL: 23, Liast Sequence update)
01-OGT-2003 (TERMELTEL: 25, Liast annotation update)
Metalloproteinase (Fragment).
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136 ELLRDPSLGAQFRVHLVYOVVILTEPEGAPNITANLTSSLLSVÇGWSQTINPEDDTDPGHA 195
                                                                        REXXHPSIRNSVSEVVVKILVIXBBOKGPBVTSNAALTERNFCRWOKOHNPPSDRDABHY 142
                                                                                                                                                                  DLVLYITRFDL---BLPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHBIGHS 252
                                                                                                                                                                                                                                                                                                                                              FGLEHDGAPG----SGCGPSGHVMAS-----DGAAPRAGLAWSPCSRRQLLSLLSAGRAR 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 SRICGGGVQYIMRECDNPVPKNGGKYCEGKRVRYRSCNIBDCPDNNGKIPREEQC-EASN 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 QPLRSSPGGASFYHWGAAVPHSQGDALCRHMCRAIGESFIMKRGDSFLDGTRCMPSGPRE 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 EFSKASFGSGPAVEWTPKYAGVSPKDRCKLICQAKGIGYFFVLQPKVVDGTPCSP---- 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 DGTLSLCVSGSCRIFGCDGRMDSQQVWDRCQVCGCDNSTCSFRKGSFTAGRAREYVTFLT 598
                                                                                                                                                                                                                                                    DTAILFTRODICGAQTCD----TLOMADVGTICDPSRSCSVIEDDGLQAAFTTAHBLGHV
                                                                                                                                                                                                                                                                                                                                                                                                                               PNMPHDDAKOCASINGVNRDSHMMASMLSNLDRSQP-----WSPCSAYMITSFLDNGHGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVWDPPRPQPGSAGHPPDAQPGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 CLMDKPQ----SPIQLPSDLPGTLYDANRQCQFTFGBESKHCPDA---ASTCTTLWCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 SGGILVCQTKHPPWADGTSCGEGRWCVNGKCVNKTDRKHFDTP----VHGSWGPWGPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 DST-SVCVOGOCVKAGCDRIIDSKKKFDKCGICGGNGSTCKKISGSVTSAKP-GYHDIVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       553 VALTEDRIPRIBEIRINGPLOEDADIQVYRRYGEEYGNLTRPDITFTYFQPKPRQA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         645 PIFSEWVIEEW----GECSKSCGQG-W------QRRLVECRDING--QPASECAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PAMPEACVLEPCPPYMAVGDFGPCSASCGGGLRERPVRCVEAGGSLLKTLPPARCRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            964 PLDOSSCSRLLVPLLDGTECGVEKWCSKGRCRSLVEL----TPIAAVHGRWSSWGPRSPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       688 VKPASTRPCADLPC-PRWQLGDWSPCSKTCGKGYKKRTLQCLSHDGGVL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   736 -----SQESCDPLXXPKHY 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q94493 PRELIMINARY;
Q94693;
01-MAY-2000 (TERMELTE1.13,
01-CCT-2002 (TERMELTE1.22,
01-CCT-2003 (TERMELTE1.25,
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STRAIN=Berkeley; WEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., HOLt R.A., Evans C.A., Gocayne J.D.,

SEQUENCE FROM N.A.

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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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371 WITHAKKKRPARGSRGCGDQPCPAHWWPGPWQPCPVITC-----RPVGPV-----AP 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 ELLRDPSLGAQFRVHLVKAVILTEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 RLYKHPSIRNGVSLVVVVXILVIHDEQKGPEVTSNAALTLRNFCMAGKGHNPPSDREHY 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 GLEHDGAPG----SGCGPSGHVWAS-----DGAAPRAGLAWSPCSRRQLLSLLSAGRARC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408 NMPHDDAKQCASINGVNQDSHMASMISNLDHSQP----WSPCSAYMITSFLDNGHGEC 462
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                                                      748 ---QGSQQPPAMPEACVLEPCPPYWAVGDFGPCSASCGGGLRERPVRCVEAQGSLLKTLP 804
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11.74; Score 906; DB 4; Length 967;
Best Low Similarity 29:64; Pred. No. 4.78-62;
Conservative 111; Mismatches 320; Indels 134; Gaps
Matches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
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PROSITE: P800142; ZIVC_PROTEBASE; 1.
BYDODELICAL PEOCHER.
SEQUENCE 967 AA: 105387 WW: FFID399674201C3D CRC64;
                                                                                                                                                                                                                                                                                                                               016 PORRESVVCLDEHDVVVADAECGHLOKPAEMEPCESS 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                             805 PARCRA----GAQQPAVALETCNPQPCPARWEVSEPS 837
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SMART; SMOOGOB; TSEL; 3.
PROSITE; PSSO215; ADAM MEPRO; 1.
PROSITE; PSSO265; CYTOGHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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01-0CT-2002 (TEMBLEE). 22,
01-0CT-2002 (TEMBLEE). 22,
01-0CT-2003 (TEMBLEE). 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
Homo sapiens (Human).
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QBNE26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               640 CSRSGGGGVSTQQRECDNPVPANGGVPCIGERKRYKICRKRPCPAEEPSFRAQQCARFD- 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 -GINNAMCIDGICKKVQCDMIVDSBVQDDRCGVGGSGDQQDPVRETYIDPPAAKDGAYVE 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 596 FLTVTPNLTSVYIAN--HRPLFTHLAVRIGG-RYVVAGKØSISPNTTYPSLLEDGRVEYR 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 INTIPARARHILIRELANSPHFLAIATGDGGDRFYLMGDSLIS----BPG-----BPE 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553 VALTE---DRIPRIEEIRIWGPLQEDADIQVYRRYGEE----YGNLTRPDITFTYFQPKP 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 IAGAESLYDRVDEOETÍTIPOPIOHSISLYALVRGNESNAGIPYEFTLPALNVTAGROPO 914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 WRLSNWTA----CSASCGGGVQHREPICQENGKGESNEPPQRIVSIKRNLLIALGDTLPC 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 RVPHTKFKYETQPQTEPDHAEIPRRRSISSPRHVETLI-VADATMSAFHRDLNGYLLTI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 INIGAELLEDPSLGAQPRVHLVKKVILTEPEG--APNITANLTSSLLSVCGWSQTINPED 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 MANYSALYKDPSIGNSIELVVVRIIOLDEEBSOLOLNITONAOKNIDRFCSWOHKLNKGS 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 SCHTDPLDQSSCGRLLVPLLDGTECGVBKWCSKGRCRSLVELTPIAAVHGRWSSWGPRSP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 CSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLBFMSQQCARTDG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      479 QPLRSSPGGASFYHWGAAVPHSQGDALCRHMCRAIGESFIMKRGDSFLDGTRCMPSGPRE 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 DIDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPPSPGFQRQ------RQRRAAGGILHLELLVAVGPDVFQAHQEDTERYVLTW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1059,
Query Match 11.7%, Score 907.5, DB 5, Best Local Similarity 30.4%; Pred. No. 4.1e-58; Best Local Similarity 105; Mismatches 341,
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6 a 590BE2B0E73740FF CRC64;

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900 AA; 100679 NW;
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                                    Similarity
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01-OCT-2003
                                                 Matches 226;
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463 IMDKPQ-----NPIQLPQDLPQDARQCQFTPQEDSKHCPDA---ASTCSTLWCT 512
                                                                                                               628
                                                                                                                                      DGQPLRSSPGGASFYHWGAAVPHSQGDA---LCRHMCRAIGESFIMKRGDSFLDGTRCMP 533
                                                                                                                                                                                       534 SGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRARBY 593
                                                                                                                                                                                                                 584 ---STDST-SVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTCKKISGSVTSAKP-GY 738
                                                                                                                                                                                                                                        594 VTFLIVIPNLISVYIANH-----RPLFTHLAVRIG-GRYVVAGKMSISPNTIYPSLLEDG 647
                                                                                                                                                                                                                                                               739 HDIITIPTGATNIEVKQRNQRGSRNNGSFLAIKAADGTYILNGDYTLS-----TLEQDI 792
                                                                                                                                                                                                                                                                                         548 RVEYRVALTEDRIPRIBEIRIMGPLQEDADIQVYRRYGEBYGNLTRPDITFTYFQPKPRQ 707
                                                                                                                                                                                                                                                                                                                   793 MYKGVVLRYSGSSAALBRIRSFSPLKEPLTIQVL----TVGNALRPKIKYTYFVKKKKE 847
                                                                                                                                                                                                                                                                                                                                          -----AWV---WAAVRGPCSVSOGAGLRWVNYSCLDQARKELVETVQCQGSQQP-- 753
                                                                                                                                                                                                                                                                                                                                                                 348 SPNAIPTFSAWVIEEW----GECSKSCELG--W------QRRLVECRDING--QPAS 890
                                                                                                                                                                                                                                                                                                                                                                                           154 -----PAWPEACVLEPCPPYMAVGDFGPCSASCGGGLRERPVRCVEAQGSLLKTLPPA 806
                                                                                                                                                                                                                                                                                                                                                                                                                     891 ECAKEVKPASTRPCADHPC-PQWQLGEMSSCSKTCGKGYKKRSLKCLSHDGGVL---- 943
                                      162 TDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRCRSLVEL----TPIAAVHGRWSSWGPRS 417
                                                                                       PCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQABMCNTQAC-EKTQLEFMSQQCART 476
                                                                                                                                                                529 HNEFSKASFGSGPAVEW---IPKYAGVSPKDRCKLICQAKGIGYFFVLQPKVVDGTPC-- 683
                                                                                                            570 DCSRTCGGGVQYTWRBCDNPVPXXGGKYCBGKRVRYRSCNLBDCPDNNGKTFRBEQC-BA
                                                             GTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTDRKHFDTPF---HGSWGMWGPWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 900 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                            807 RCRAGAGOPAVALETCNPOPCP 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      944 ----SHESCDPLKKP 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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01-OCT-2002 (
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DGRVEYRVALTEDRIPRIEEIRIMGPLQEDADIQVYRRYGEEYGNLTRPD-----ITFT 699
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                                                                                                                                                                                                                                                           205 RSTERGAPRENEVLMITRKRDLARPHLHHD-------NFHL---GPSQKQHF 246
                                                                                                                                                                                                                                                                                                                                           CLQAL----EPQAVSSYLSPGAPLKGRPPSPGFQRQRQRQRRAAGGILHLELLVAVGPDV 115
                                                                                                                                                                                                                                                                                                                                                                                                                            247 CGRRKKYMPQPPNDDLYILPD-----EYKPSSRHKRSLLKSHRNEELNVETLVVVDRKM 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 FQAH-QEDTERYVLTNINIGAELLEDPSLGAQFRVHLVRWVILTEPEGAPNITANLTSSL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 MOSHGHENITTYVIJILNAVSALFKDGTIGGNINIVIVGLILLEDEOPGLAISHHADHTL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 LSVCGWSQTINPEDDTDPGHADLV--LYITRFDLELPDGNRQVRGVTQLGGACSPTWSCL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 TSFCQWQSGLMGKDGTRHDHAILLTGLDICSWKNBPCD----TLGFAPISGMCSKYRSCT 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 ITEDTGFDLGVTIAMEIGHSPGLEHDGAPGSGGGPS-GHVMASDGAAPRAGLAMSPCSRR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417 VNEDSGLGLAFTIANESGENFGWVHDG-EGNMCKKSEGNIMSPILAGRAGVFSWSSCSRQ 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 QLISLISAGRARCVWDPPRPQPGSAGHPPDAQPGLYYSANEQCRVAFGPKAVAC--TPAR 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 YLHKFLSTAQAICLAD--QPKPVKBYKYPBKLPGQLYDANTQCKWQPGBKAKLCMLDPRK 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 EHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRCRSLVELTPIAAVHGR 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 ---DICKALWCHR---IGRKCETKFMPANECTLCGQDMMCRGGQCVKYGDEGP-KPTHGH 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 WSSWCPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLEFM 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587 WSDWSPWSPCSRTCGGGISHRDRLCTNPRPSHGGKFCGGSTRTLKLCNSORCPLDSVDFR 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 SQQCARIDGQPLRSSPGGASPYHWGAAVPHSQ--GDALCRHMCRAIGESFIMKRGDSFLD 527
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                                                                                                                                                                 3 RPTRPKAPSHSAPLL---GLALLRWHORHPRARCPPLCVAGILACGFLLGCWGPSHFQQS 59
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bikaryota, Merazos, Chordata, Cramiata, Vertebrata, Buteleostosi,
Boridae, Borinae; Cetartiodactyla; Ruminantia; Pecora; Bovoidea,
WCB_EATIS-9913;
10.6%; Score 819.5; DB 11; Length 900;
llarity 29.6%; Pred, No. 1.1e-51;
Conservative 105; Wismatches 306; Indels 127;
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11-0CT-2003 (TERMELrel. 25, Last sequence update)
11-0CT-2003 (TERMELrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 GPQVGPSAAQTLRSFCAWQRGLNTPDDADPGHFDTAILFTRQDL-CGVSTCDTLGMADVG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACSPTWSCLITEDIGFDLGVTIAHEIGHSFGLEHDGAPGSGC----GP---SGHVMASD 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337 TVCDPARSCAIVEDDGLQSAFTAAHELGHVFSNLHDNS--KQCTGLNGPESTSRHVMAPV 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 GAAPRAGLAWSPCSRROLLSLISBAGRARCVWDPPRPQPGSAGHPPDAQPGLYYSANBQCR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 VAPGPKAVACTPAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRCR 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLVEL----TPIAAVHGRMSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADL 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             508 HVDQLQAFNVPQAGGNGPNGSMG---DCSRSCGGGVQFSSRDCTRPVPRNGGKYCEGRRT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAEMCNIQACEK-IQLEFMSQQCA----RIDGQPLRSSPGGASFYHWGAAVPHSQGDA-- 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        565 RFRSCNÍQDCPIGSALIFREBQCAAYNHRID--LFKNFPGPMD---W---VPRYIGVAPR 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LCRHMC--RAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDS 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 DOCKLICQIRALGYYYUL--DPRVADGIPCSPD-----SSSVCVQGRCHHAGCDRVIGS 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 KKKPDKCMVCGGDGSSCSKQSGSFKKFR-YGYNNVTIPAGATHILVRQQGSPSVRSLYL 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         609 ANHRPLFTHLAVRIGGRYVVAGRASISPNTTYPSLLEDGRVEYRVALTEDRLPRLEEIRI 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           728 ALKLP------DGSYALNGEYTLIPSPT--DVVLPGAVSLRYS---GATAASETLSG 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQVWDRCQVCGGDNSTCSPRKGSFTAGRAREYVTFLTV------TPNLTSVYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 LHLELLVAVGPDVFQAHQEDTERYVLTNLNIGABLLRDPSLGAQFRVHLVKMVILTEPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 RPVETLVVADDXMAAPHGAGLKRYLLTVMAAAAKAFKHPSIRNPVSLVVTRLVVLGPGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 MAHVDPEEPWSPCSARFITDFLDNGFGHCLLD----KPEAPLHLPVTFPGKDYDADRQCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 LIFGFDSRHCP---QLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGGRCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Query Match

1.84; Score 759.5; DB 6; Length 839;
Best Local Similarity 31.44; Pred. No. 766-47;
Matches 219; Conservative 85; Mismatches 289; Indels 105;
                                                                                          ċ
                           Segiornes present D., Annie B., Colline-Bacie L., Corcoren Distance Carle F. Mortie C. Driver. A. Lafwille E.; St. Driver. B. Driver. Segiorne. C. Driver. Brit. Condens. Driver. Brit. Br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     669 WGPLQEDADIQVYRRYGEEYGNLTRPDITFTYFQPKPR 706
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10-70-700 (TEPBELEN 1.2) Create update)

0.07-7000 (TEPBELEN 1.2) Last sequence update)

0.07-7001 (TEPBELEN 1.2) Last monoiston update)

1.07-7001 (TEPBELEN 1.2) Last monoiston update)

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PRELIMINARY;

08K384; Q8K384

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LOALEPGAVSSYLSPGAPLKGR------PPSPGFQRQRQRQRAAGGI 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 GPOVGPSAAGTIRSFCTWORGLATPNDSDPDHFDTAILFTRODL-COVSTCDTLGMADVG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 TVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHDNSKPCTNLNGQG-GSSRHVMAPVM 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 AAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQPGBAGHPPDAQPGLYYSANBQCRV 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 448 TFGPDSSHCP---OLPPPCAALWCSGHINGHAMCOTKHSPWADGTPCGSSQACMGGRCLH 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDOLKDENVPOA---GGWGPWGPWGDCSRTCGGGGVOFSBRDCTRPVPRNGGKYCEGRRTR 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEMCNIQAC-EKTQLEFMSQQCA----RIDGQPLRSSPGGASFY-HWGAAVPHSQGDALC 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCMVCGSDGSRCSKQSGSPKKFR-YGYSDVVTIPAGATHILVRQQGGSGLKSIY--LALK 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 IMLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVXAVILTEPEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 REVETLAVADDKAARHGTGLKRYLLTAMAAAKAFKHPSIRNPANLAVTRLVILGSGOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 APNITANLISSLLSVCGWSQTINPEDDIDPGHADLVLYITRFDLELPDGNRQVRGVTQLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
Bukaryota; Merazoa; Chordata; Cranista; Vertebrata; Buteleostomi;
Mammila; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mes
NCBI_TRAID=10930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 833;
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Best Local Similarity 30.58; Pred. No. 1.7e-46;
Matches 209; Conservative 92; Mismatches 303; Indels
                                                                                                       databases
                                                                                                                                                                                                                                                                                                                                                                                                                                          Integrin, Protease, MeTalloprotease.
SEQUENCE 833 AA; 90097 MM; 4CEC83DFBC3AA619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.7%; Score 748.5; DB 11
                                                                                      Strausberg R.;
Submitted (APR-2002) to the BMBL/GenBank/DDBJ
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                                                                    SEQUENCE FROM N.A.
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397 LVEL----TPIAAVHGRMSSWGPRSPCGRSCGGGGVVTRRRQCNNPRPAFGGRACVGADLQ 452 517 VDQLXDPNVPQA---GGWGPWGPWGDCSRTCGGGVQFSSRDCTRPVPRNGGKYCEGRRTR 573 453 AEMCNTGAC-EKTQLEFMSQQCA----RTDGQPLRSSPGGASFY-HWGAAVPHSQGDALC 506 574 PRSCNTENCPHGSALTFREEQCAAYNHRTD--LFKSFPGPMDWVPRYTGVAPRDGCKLTC 631 507 RHMCRAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWD 566 632 Q -- ARALGYYYVLE -- PRVADGTPCSPD -- -- TSSVCVQGRCIHAGCDRIIGSKKMFD 681 567 RCQVCGGDNSTCSPRKGSFTAGRAREYVTFLIVTPNLTSVYIANH-----RPLFTHLAVR 621 682 KCMVCGGDGSRCSKQSGSFKKFR-YGYSDVVTIPAGATHILVRQQGGGGLKSIY--LALK 738 622 IG-GRYVVAGKMSISPNTTYPSLLEDGRVEYRVALTEDRLPRLEEIRIWGPLQEDADIQV 680 739 ISDGSYALNGEYTLMPSPT--DVVLPGAVSLRYS---GATAASETLSGHGPLAQPLTLQV 793

404 AHVDPEEPWSPCSARFITDPLDNGYGHCLLD----KPEAPLHLPATFFGKDYDADRQCQL 459 337 AFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRCRS 396 460 TPGPDSSHCP---QLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGSSQACMGGRCLH \$16

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522 IG-GRYVVAGRMSISPNTTYPSLLEDGRVEYRVALTEDRLPRLEEIRIMGPLQEDADIQV 680
                                                                                          727 LSDGSYALNGEYTLMPSPT--DVVLPGAVSLRYS---GATAASETLSGHGPLAQPLTLQV 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Būkaryota, Metazoā, Chordata, Craniata, Vertebrata, Euceleostori,
Mommalia, Eucheria, Rodentia, Scurognathi, Muridae, Murinae, Mus.
NCBL_TRAID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match Berliniarity 9:74; Score 748.5; DB 11; Length 845; DB best Local Similarity 30:3; Preci. No. 179-46; Matches 209; Conservative 92; Mismatches 303; Indels 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TremBirel. 23, Created)
(TremBirel. 23, Last sequence update)
(TremBirel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 845 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A disintegrin-like and metalloprotease.
                                                                                                                                                                                     581 YRRYGERYGNLTRPDITFTYROPKP 705
                                                                                                                                                                                                                                            782 L----VAGNPQNARLRYSFEVPRP 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (
01-MAR-2003 (
01-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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345 TVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHDNSKPCTNLNGQG-GSSRHVMAPVM 403

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61 LQALEPQAVSSYLSPGAPLKGR------PPSPGPGRQRQRQRAAGGI 102 170 LOPLEGGALNSAGGPGAHILRRKSPASSOGPMCTVKAPSGSPSP----ISRRTKRFASLS 22S 103 LHLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVGVVILTEPEG 162 226 RPVETLVVADDKMAAFHGTGLKRYLLTVMAAAAKAFKHPSIRNPVNLVVTRLVILGSGQE 285

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81; Gaps

94 L----VAGNPONARLRYSFFVPRP 813 Search completed: March 13, 2004, 07:43:13 Job time : 147.125 secs

681 YRRYGEEYGNLTRPDITFTYFQPKP 705

A

80153 Human ADA	153 Aau8(AAUBO	1224	4	147.	Ç2
9500 Human	500 A	7795	1170	14.8	1147.5	44
50762 Novel	762 A	ADAS 07	1224	÷	148.	43
33432 Hum	132 Abr	ABR83		÷	148.	23
72431 Novel	31 Abg		1224	4	ę,	7
497 Human	2.4	AAU7		÷	ę. 9	0
254 Human	54	AA015		4	œ.	39
168	91	AAU72	1224	÷	8	38
301 Human	301	AAB72		÷	15	33
1286 Human	585	AAB72		÷	15	36
1702		ABG30		ıń.	165.	33
1173 Human	173	AAE19		'n.		34
592 Polype		ADD44	1363		17	33
1896 Human m	968	AAU72		'n	176.	35
448 Human	148	AAO14		'n		31
3703 Hum		ABG30		'n	176.	30
893	93		934	ıń.		53
5717 Human		ABG66	223	ın.		28
3113	1.3		223	ió	1185	53
688		AAU/2	1505	in		92

RESULT ABB0411 ID AI	RESULT 1 BBE04153 ID ABB04153 standard; protein; 1416 XX	tein; 1416 AA.
S X E	ABB04153; 26-MAR-2002 (first entry)	[22]
X E	Human ADANTS-M polypeptide	tide.
žž	Osteoarthritis; rheumatoid	toid arthritis; inflammatory bowel disease;
ž	Crohn's disease, asthn	Crohn's disease; asthma; Alzheimer's disease; organ transplant rejection;
28	atherosclerosis; conge	Cachexa; allergy, cancer; leukaemia; lymphona; osceoporolis; atherosclerosis; congestive heart failure; myocardial infarction; stroke;
5 %	neurodegenerative disease, aucolmmine Parkinson's; migraine; pain; depressio	neurodegenerative disease) accommune disolder; nuntingion s; Parkinson's; migraine; pain; depression; multiple sclerosis; burn;
20	intertility; diabetic A Disintegrin And Meta	interility; diabetic snock; gene inerapy; ADAMYS-M; A Disintegrin And Metalloprotease; thrombospondin domain.
183	Homo sapiens.	
á B	Total	Occupation (Cum) African
E	tide	
E	/label	The second secon
E E	/note: proces	/note= "The mature form of the ADAMTS-M procein is processed by furin cleavage of the prodomain"
FF	Cleavage-site 9497	
E	Protein 98. 1416	416
EE	/label	form of the
E		processed by furin cleavage of the prodomain"
EE	Domain 98311	98311 /label= Metalloproteage domain
E	Domain 247. 272	247. 272
:::	Domain 324.	Against a state of the state of
t	Domain 410473	# Disintegrin domain
i i	/label= T	/label= Thrombospondin_submotif 419424
E		/label= Heparin-binding_domain
: ::	Lomein 1039.	1999iise /label= Thrombospondin_submotif
ΧZ	EP1152055-A1.	
ž B	07-NOV-2001.	

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New polymucleoride, usedtil in gene therepsy, particularly for treating or preventing e.g. arthritis. Crohir disease, Althermer's disease and organ treanglant toxicity and rejection, comprises ADMMTS polymucleotide and anceded schoolepstide. Walsh RT; Wachtmann TS, Claim 4; Fig 2, 31pp; English. 24-APR-2001; 2001BP-00303706 27-APR-2000; 2000US-0200040P Mitchell PG, PFIZ) PFIZER PROD INC WPI: 2002-084275/12 N-PSDB; ABA02549. Buckbinder L,

The present sequence represents a ADMTS percent, designed ADMTS-4.

The addition the chartcersists of the ADM (a bisinegarin Add settlement and the addition of the addition of the ADMTS-4.

ADMTS-4. The administration designed as and constant and settlement and constant and settlement and administration of the administration of

Sequence 1416 AA;

09 Gaps .; o DB 5; Length 1416; 0; Indels 0; Mismatches Score 7751; Pred. No. 0; 100.0%; Conservative Best Local Similarity Matches 1416; Conserv Query Match

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120 120 180 180 240 240 300 09 LGVTIAHEIGHSFGLEHDGAPGSGCGPSGHVMASDGAAPRAGLAWSPCSRRQLLSLLSAG 300 PGRPTRPKAPSHSAPLLGLALLRMHQRHPRARCPPLCVAGILACGFLLGCWGPSHFQQSC PGRPTRPKAPSHSAPLLGLALLRNHQRHPRARCPPLCVAGILACGFLLGCWGPSHFQQSC LOALEPOAVSSYLSPGAPLKGRPPSPGFORORORRAAGGILHLELLVAVGPDVFQAHQ LOALEPQAVSSYLSPGAPLKGRPPSPGFQRQRQRRAAGGILHLELLVAVGPDVFQAFQ EDTER YVLTNIMIGAELLR DPSLGA OPR VHLVKAVILTEPEGA PNITANLTSSLLSVCGM BOTERYVLTNINIGABLIRDPSLGAOFRVHLVKKVILTEPBGAPNITANLTSSLLSVCGW SQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFD SOTINPEDDTDPGHADLVLYITRFDLELPDGNROVRGVTOLGGAGSPTWSCLITEDTGFD LGVTIAHEIGHSFGLEHDGAPGSGCGPSGHVMASDGAAPRAGLAWSPCSRRQLLSLLSAG 61 19 21 121 81 181

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SAGGAGLALENETCVPGADGLEAPVTEGFGSVDEKLPAPEPCVGMSCPPGWGHLDATSAG 900 841 SAGGAGLALENETCVPGADGLEAPVTEGPGSVDEKLPAPEPCVGMSCPPGWGHLDATSAG 900 CGGGLRERPVRCVEAGGSLLKTLPPARCRAGAGQPAVALETCNPQPCPARWEVSEPSSCT SCGAGLRWYNYSCLDQARKELVETVQCQGSQQPPAWPEACVLEPCPPYWAWGDFGPCSAS CGGGLRERPVRCVEAQGSLLKTLPPARCRAGAQQPAVALETCNPQPCPARWEVSEPSSCT 721 781 781

780 780 840 840

SCGAGLRWWYSCLDQARKELVETVQCQGSQQPPAWPBACVLBPCPPYWAVGDFGPCSAS

a ò g ò 음 Š Q, ŝ 용 EKAPSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGIMBLRFLCMDSALRVPVQEBLCGLAS 960 901 EKAPSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGLMELRFLCMDSALRVPVQEELCGLAS 960 KPGSRREVOQAVPCPARWQYKLAACSVSOGRGVVRRILYCARAHGEDDGEEILLDTQCQG 961 KPGSRREVCOAVPCPARMOYKLAACSVSCGRGVVRRILYCARAHGEDDGEBILLDTQCQG LPRPEROBACSLEPCPPRWKVMSLGPCSASCGLGTARRSVACVQLDQGQDVBVDEAACAA 901 961 1021 ò a ò a ò

1080

1021 LPRPEPQEACSLEPCPPRWKVMSLGPCSASCGLGTARRSVACVQLDQGQDVEVDEAACAA

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LVRPEASVPCLIADCTYRWHVGTWMECSVSCGDGIQRRRDTCLGPQAQAPVPADFCQHLP 1140 DCAVAIGRPIGEVUTLRVLESSINCSAGDMILLWGRLTWRKMCRKLLDWTFSSKTNTLVV 1260 1081 LVRPEASVPCLIADCTYRWHVGTWNECSVSCGDGIQRRRDTCLGPQAQAPVPADFCOHLP KPVTVRGCWAGPCVGQGTPSLVPHERAAPGRTTATPAGACGRQHLEPTGTIDMRGPGQA 1141 KPVTVRGCWAGPCVGQGTPSLVPHEBAAAPGRTTATPAGACGRQHLEPTGTIDMRGPGQA 1081 1141 1201 ò a ò g à

1200

EGFLKAQASLRGQYWTLQSWVPEMQDPQSWKGKEGT 1416 1381 BGFLKAQASLRGGYWTLQSWVPBWQDPQSWKGKBGT

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360 360

RARCVWDPPRPOPGSAGHPPDAOPGLYYSANEOCRVAFGPKAVACTFAREHLDMCQALSC RARCVWDPPRPQPGSAGHPPDAQPGLYYSANEQCRVAPGPKAVACTFARBHLDMCQALSC

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The investing varies to an anisotied or managementially pure two will altered faces or cleaving processes (VeP-p) polyperides, VeP-p as useful for the investing for the investigation in the i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 PSPGFQRQRQRQRRAAGGILHLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSPGFQRQRQRRAAGGILHLELLVAVGPDVFQANGEDTERYVLTNINIGAELLRDPSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 GAQFRVHLVKAVILIEPEGAPNITANLISSLLSVCGWSQTINPEDDIDPGHADLVLYITR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GAÇERVHLVKAVILTEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDFGHADLVLYITR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 PDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPGS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 GCGPSGHVMASDGAAPRAGLAWSPCSRRQLLISLLSAGRARCVWDPPRPQPGSAGHPPDAQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GCGPSGHVMASDGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQPOSAGHPPDAQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 PGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 3B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGLYYSANEQCRVAFGPKAVACTPAREHLDMCQALSCHTDFLDQSSCSRLLVPLLDGTEC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 GVEKWCSKGRCRSLVELTPIAAVHGRMSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGG 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 GVEKWCSKGRCRSLVELTPIAAVHGRWSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 RACVGADIQAEMCNIQACEKIQLEFMSQQCARIDGQPLRSSPGGASFYHWGAAVPHSQGD 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504 ALCRHMCRAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQ 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 VWDRCQVCGGDNSTCSPRKGSFTAGRAREYVTFLTVTPNLTSVYIANHRPLFTHLAVRIG 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541 VMDRCQVCGGDNSTCSPRKGSFTAGRAREYVTFLTVTPNLTSVYIANHRPLFTHLAVRIG 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGBEYGNLTRPDITFTYFOPKPROAWWAAVRGPCSVSCGAGLRWUNYSCLDQARKELVE 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MHORHPRARCPELCVAGILACGFLIGCHGPSHFQQSCLQALEPQAVSSYLSPGAPLKGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 FDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444 RACVGADLQAEMCNIQACEKTQLEFMSQQCARIDGQPLRSSPGGASFYHWGAAVPHSQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 ALCREWCRAIGESFIMKRGDSFIDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 GRYVVAGKMSISPNTTYPSLLEDGRVEYRVALTEDRLPRLEEIRIWGPLQEDADIQVYRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGEBYGNLTRPDITFTYFQPKPRQAWVAAVRGPCSVSCGAGLRWVNYSCLDQARKELVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 MHORHPRARCPPLCVAGILACGFLLGCWGPSHFQQSCLQALEPQAVSSYLSPGAPLKGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.1%; Score 7604; DB 5; Length 1427; 97.6%; Pred. No. 0;
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l: Fiq 5; 93pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 1427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Claim
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                                                                                                                                                                                                                                              Haman, Von Wiltehrand factor-cleaving processes vWF-pp, therapy, ensymes, transpenic animal; immunisation; thromboeneous precedingsia, intromotoric thromboeytic purpura; TPP; Wencoh-selected to preceding intromotoric structura; TPP; Wencoh-selected to processes intromotoria; Intromotoria; Intromotoria; Intromotoria; Processes, Introdoceous; Arangenic anticosagisan; Chromosome 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laemmie B. Gerritsen HS. Furlan M. Turecek P. Schwarz B. Schefflinger F. Antoine G. Kerschbaumer R. Tagliavacca I Zimmerann K. Voelkel D.
                                                                                                                                                                                                    Human Von Willebrand factor-cleaving protease (vWF-cp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Mature human vWF-cp protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Thromspondin type I motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Thromspondin type I motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Thromspondin type I motif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "note= "Distintegrin like motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "note= "Cysteine rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9. .75
note= "Furin cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224. .228
/note= "Catalytical side"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .51
/label= Signal_peptide
                                                                 AAE24450 standard; protein; 1427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Met turn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-NOV-2000; 2000US-00721254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-2001, 2001WO-EP013391
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producing a purified human aggrecanase protein which can be used
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                                                                                                 Agostino MJ,
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Matches 1392; Conserv
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                                        ALCRHMCRAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDSGO 540
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1370 SESSQAEMEPSEGFLKAQASLRGQYWTLQSWVPEMQDPQSWKGKEGT 1416
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2000US-0257803P.
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N-PSDB, ABQ75946.
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Ramkumar J, Thi
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05-JAN-2001;
19-JAN-2001;
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Query Match 93.8%; Best Local Similarity 96.1%; Matches 1338; Conservative Sequence 1445 AA;

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SPGAPLKGRPPSBGRQRQRQRRAAGGILHIELLVAVGPDVPQAHQEDTERYVLTNINI 133
                                                                                                                                              SPSPP-PGRPSPGFORORORANGGILHLELLVAVGPDVFOAHQEDTERYVLTNINI
                                                         4, Indels 50;
93.8%; Score 7274; DB 5; Length 1445;
96.1%; Pred. No. 0;
ive 0; Mismatches 4; Indels 50
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Human PMMM Incyte ID 7473607CD1 (first entry)

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possesse, useful for producing preparation for therapy of thrombosia and 
thromboseabild disease such as thrombotic thromboytic purpura.
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                                     1194 YVLSSFLSGSCCRRGACGRQBLEPTGTIDWRGPGGADCAVAIGRPLGEVVTLRVLESSLN
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Kerschbaumer R, Tagliavacca L;
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Scheiflinger F, Antoine G,
Zimmermann K, Voelkel D,
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                                     GABLLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDPG
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                                                                                                                                                       HADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSF
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                                                                                                                                                                                                                                                                              GLEHDGAPGSGCGPSGHVMASDGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQP
                                                                                                                                                                                                                                                                                                                                       234 GLEHDGAPGSGCGPSGHVMASDGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQP
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Best Local Similarity Matches 1319, Conserv Sequence 1353 AAs

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                                                                1058 RSVACVQLDQGQDVEVDEAACAALVRPEASVPCLIADCTYRWHVGTWMECSVSCGDGIQR
                                                                                              RSVACVQLDQQQDVEVDEAACALVRPEASVPCLIADCTYRWHVGTWMBCSVSCGDGIQR
                                                                                                                                                 118 RRDTCLGPQAQAPVPADFCQHLDRPVTVRGCWAGPCVGQGTPSLVPHERAAAPGRTTATP
                                                                                                                                                                                1021 RRDTCLGPQAQAPVPADPCQHLPXPVTVRGCWAGPCVGQGTPSLVPHEBAAAPGRTTATP
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2001JP-00227510.
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28-SEP-2001;
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    hatemolytic-ureantic syndrace, wFF-op can also be used for processing 
plasmatic or recombinantly produced wFF. The invention is useful for 
construction appression by Systems and generating transgenic animals which 
express the polypopide in vivo. The present sequence is human wFF-op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACVLEPCPPYWAVGDPGPCSASCGGGLRERPVRCVEAGGSLLKTLPPARCRAGAQPAV
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                                                                                                                                                                                                                                                                                               AAGGILHLELLVAVGPDVPQAHQEDTERYVLTNINIGAELLRDPSLGAQPRVHLVKKVIL
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Pred. No. 0;
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larity 97.5%;
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Gaps 34; 92.8%; Score 7190; DB 6; Length 1353; 97.5%; Pred. No. 0; Indels ö Local Similarity Sequence 1353 AA; Query Match

157 AAGGILHLELLVAVGPDVFQAHQEDTERYVLTNINIGAELLRDPSLGAQPRVHLVXXVIL 0; Mismatches Matches 1319; Conservative 86

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217 TEPECA PNITANLISSLISVCGWSQTINPEDDIDPGHADLVLYITRPDLELPDGNRQVRG 120 9 TEPEGAPNITANLISSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGWRQVRG VIQLGGACSPIWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPGSGCGPSGHVMASDGA AAGGILHLELLVAVGPDVFQAHQEDTERYVLTNINIGAELLRDPSLGAQFRVHLVRVVIL 58 18

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VIQLGGACSPIWSCLITEDIGFDLGVTIAHBIGHSFGLEHDGAPGSGCGPSGHVMASDGA APRAGLAWSPCSRROLLSLISAGRARCVWDPPRPQPGGAGHPPDAGPGLYYSANEQCRVA 278

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VELTPIAAVHGRWSSWGPRSPCSRSCGGGVVJTRRRQCNNPRPAFGGRACVSADLQAEMCN VELTPIAAVHGRWSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCN 868 108

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> TOACEKTOLEPMSOCCARTDGOPLRSSPGGASFYHWGAAVPHSQGDALCRHMCRAIGESF 361 538

toacektolepmsoccartogoplesspogaspyhwgaavphsosdalcrhmcraigesp INKREDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNST IMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNST CSPRKGSFTAGRAREYVTFLITVTPNLTSVYIANHRPLFTHLAVRIGGRYVVAGKMSISPN 518 421

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CSPRKGSPTAGRAREYVTFLTVTPNLTSVYIANHRPLFTHLAVRIGGRYVVAGKMSISPN TIYPSILIEDGRVEYRVALTEDRIPRIERIRIMGPLOEDADIOVYRRYGEBYGNLTRPDIT TTYPSILEDGRUSYRVALTEDRIPRIBEIRIMGPLQEDADIQVYRRYGEEYGNLTRPDIT 81 638 541

PTY FORKPROAW/WAAVRGPCSVSCGAGLRWVNYSCLDQARKELVETVQCQGSQQPPAWP PTYPOPKPROAWWAAVRGPCSVSCGAGLRWVNYSCLDQARKELVBTVQCQGSQQPPAMP 869 601

BACVLEPCPPYWAVGDPGPCSASCGGGLRERPVRCVBAQGSLLKTLPPARCRAGAQQPAV 720 BACVLEPCPPYMAVGDFGPCSASCGGGLRERPVRCVEAGGSLLKTLPPARCRAGAQQPAV ALETCNPOPCPARMEVSEPSSCTSAGGAGLALENETCVPGADGLEAPVTEGPGSVDEKLP 158

LR FLCMDSALRVPVOBELCGLASKPGSRBVCOAVPCPARMOYKLAACSVSCGRGVVRRI 997 ALETCNPOPCPARWEVSEPSSCTSAGGAGIALENETCVPGADGLEAPVTEGPGSVDEKLP 781 APEPCVGMSCPPGWGHLDATSAGEKAPSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGLME APEPCVGMSCPPGWGHLDATSAGEKAPSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGLME 938 721 878

841 IRFLCMDSALRVPVQBELCGLASKPGSRREVCQAVPCPARNOYKLAACSVSCGRGVVRRI

1117 1140 1020 1057 LYCARAHGEDDGEETLLDTQCQGLPRPPPPQEACSLEPCPPRWKVMSLGPCSASCGLGTAR RSVACVQLDQQQDVEVDEAACAALVRPEASVPCLIADCTYRHHVGTWMECSVSCGDGIOR RRDITCLGPQAQAPVPADPCQHLPKPVIVRGCWAGPCVGQGTPSLVPHEEAAAPGRITATP 1021 REDICIGROAQAPVPADFCQHLPRPVTVRGCWAGPCVGQGTPSLVPHEBAAAPGRITATP -----ACGROHLEPTGTIDMRGPGGADCA AGASLEWSGARGLIPSPAPGPRRLLPGFQENSVOSSACGROHLEPTGTIDMRGPGGADCA LYCARAHGEDDGBEILLDTQCQGLPRPEPQEACSLEPCPPRWKVMSLGPCSASCGLGTAR 1058 RSVACVQLDQQQDVEVDEAACAALVRPEASVPCLIADCTYRWHVGTWMECSVSCGDGIQR L178 AG-----106 961 1118 180 966

1204 VAIGRPIGEVVTLRVLESSINGSAGDMILLMGRLTWRKWCRKILDMTFSSKTNTLVVROR 1141 VAIGRPIGEVUTLEVLESSINCSAGDMILLMGRLTWRKMCRKILDMTFSSKTNTLVVROR CGRPGGGVLLRYGSQLAPETFYRECDMQLFGPWGEIVSPSLSPATSNAGGCRLFINVAPH 1264

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1261 ARIAIMALATHMGAGTEGANASYILIRDTHSLRTTAFHGOOVLYWESESSGAEMEFSEGF 1320 CGRPGGGVLLRYGSQLAPETFYRECDMQLFGPWGEIVSPSLSPATSNAGGCRLFINVAPH ARIAIHALATWMGAGTEGANASYILIRDTHSLRTTAFHGQQVLYWESESSQAEMEFSEGF 1201 1324

1416 LKAÇASLRGÇYWTLQSWVPEMQDPQSWKGKEGT 1353 1384 LKAQASLRGQYWTLQSWVPENQDPQSWKGKEGT RESULT 7

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Human von Willebrand factor (VWF)-cleaving enzyme-related protein Ź AAO16618 standard, protein; 1297 (first entry) 15-MAY-2003 AA016618;

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Human, protease inhibitor; gene therapy, vMP-cleaving enzyme; von Willebrand Sector-Claaving enzyme; burombocycopenic purpura), myocardal infarction; erebral infarction; arrestoressis; platelet thrombosis, stenosis.

W0200288366-A1. sapiens Homo

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37-NOV-2002

2001JP-00128342. 2001JP-0027510. 2001JP-00302977. 2002JP-00017596. 2002WO-JP004141 25-APR-2002; 25-APR-2001; 7-JUL-2001; 28-SEP-2001;

> 999 817 877 780 937 840 900

ú Nozaki KAGA) CHEMO-SERO-THERAPEUTIC RES INST Maeda H, Mimura N, 25-JAN-2002; Sociima K,

Ë Nakagaki Hamamoto T, (PI; 2003-120479/11, N-PSDB, ABT32584.

von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and supplementary therapy for, thrombotic thrombocycopenic purpura, and for enyphysing druges for e.g. myocardial interction and cerebral interction

Claim 4; Page 92-101, 144pp; Japanese.

LRFLCMDSALRVPVQEBLCGLASKPGSRREVCQAVPCPARMOYKLAACSVSCGRGVVRRI LYCARAHGEDDGBEILLDTQCQGLPRPEPQBACSLEPCPPRWKVMSLGPCSASCGLGTAR

LYCARAHGEDDGBEILLDTQCQGLPRPEPQBACSLEPCPPRWKVMSLGPCSASCGLGTAR

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6; Length 1297;

Gabs 22; IndelB ö Query Match
91.4%, Score 7081; DB
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1297; Conservative 0; Mismatches

157 98 AAGGILHLELLVAVGPDVPQAHQEDTERYVLTNLNIGAELLRDPSLGAQPRVHLVKKVIL

AAGGILHLELLVAVGPDVPQAHQEDTERYVLTNLATGAELLRDPSLGAQPRVHLVKAVIL

9

277 180 VTQLGGACSPTWSCLITEDTGPDLGVTIAHEIGHSFGLEHDGAFGSGCGPSGHVMASDGA VTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAFGSGCGPSGHVMASDGA 218

300 PGPKAVACTPAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRCRSL

457 360 VELTPI AAVHGRWSSWGPRSPCSRSCGGGVVTRRROCNNPRPAFGGRACVGADLQAEMCN 868

VELTPI AAVHGRMS SWGPRS PCSRS CGGGVVTRRRQCNNPRPARGGRA CVGADLQAEMCN TOACEKTOLEPMSQQCARTDGQPLRSSPGGASPYHWGAAVPHSQGDALCRHMCRAIGESP 661 TOACEKTOLEFMSQQCARTDGQPLRSSPGGASFYHWGAAVPHSQGDALCRHMCRAIGESF 58

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517 420 577 480 637 540 697 909 757 9 817 720 877 780 840 997

IMKRGDSPLDGTROMPSGPREDGTLSLCVSGSCRTFGCDGRMDSOOVWDRCQVCGGDNST IMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNST CSPRKGSFTAGRAREYVTFLTVTPNLTSVYIANHRPLFTHLAVRIOGRYVVAGKMSISPN 518 578

CSPRKGSFTAGRARETVTFLTVTPNLTSVYIANHRPLFTHLAVRIGGRYVVAGKMSISPN TIYPSLLEDGRVEYRVALTEDRLPRLEEIRIWGPLQEDADIQVYRRYGEEYGNLTRPDIT TYYPSLLEDGRVBYRVALTEDRLPRLEEIRIMGPLQEDADIQVYRRYGEBYGNLTRPDIT 181 538 541

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PTYPOPKPROAWWAAVRGPCSVSCGAGLRWWYSCLDOARKELVBTVOCOGSGOPPAWP FTYPQPKPRQAWWAAVRGPCSVSCGAGLRWWNYSCLDQARKELVBTVQCQGSQQPPAWP eacvlepoppymavgdpgpcsascggglrerpvrcveaggsllktlpparcragacopav 869 209 758

BACVLEPCPPYWAVGDPGPCSASCGCCLRERPVRCVBAGGSLLKTLPPARCRAGAQQPAV ALETCNPOPCPARWEVSEPSSCTSAGGAGLALENETCVPGADGLEAPVTEGPGSVDEKLP ALETCNPOPCPARWEVSEPSSCTSAGGAGLALENETCVPGADGLEAFVTEGFGSVDEKLP APEPCYGMSCPPGWGHLDATSAGEKAPSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGLME 561 318 757 878

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APEPCVGMSCPPGWGHLDATSAGEKAPSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGLME LRFLCMDSALRVPVOEELCGLASKPGSRREVCQAVPCPARMQYKLAACSVSGRGVVRRI

938

Claim 4; Page 102-111; 144pp; Japanese

1178 1357 1238 TAFHGQQVLYWESESSQAEMEFSEGFLXAQASLRGQYWTLQSWVPEMQDPQSWKGKEGT 1416 1297 -GACGROHLEPTGTIDMRGPGQADCAVAIGRPLGEVVTLRVLESSINCSAGDMLLLWGRL TWRKWCRKLLDMTPSSKTNTLVVRQRCGRPGGGVLLRYGSGLAPETFYRECDMQLFGPWG BIVSPSLSPATSNAGGCRLFINVAPHARIAIHALATNMGAGTEGANASYILIRDTHSLRT RSVACVQLDQGQDVEVDEAACAALVR PEASVPCLIADCTYRWHVGTWMECSVSCGDGIQR RRDTCLGPQAQAPVPADFCQHLPKPVTVRGCWAGPCVGQGTPSLVPHBBAAAPGRTTATP TWRKNCRKLIDMTPSSKTNTLVVRQRCGRPGGGVLLRYGSQLAPETFYRECDMQLPGPWG BIVSPSLSPATSNAGGCRLFINVAPHARIAIHALAINMGAGTEGANASYILIRDIHSLRI RSVACVQLDQGQDVEVDEAACAALVR PEASVPCLIADCTYRWHVGTWWECSVSCGDGIQR REDITCLGPQAQAPVPADPCQHLPRPVTVRGCWAGPCVGQ-----1178 AGACGRQHLEPTGTIDMRGPGQADCAVAIGRPLGEVVTLRVLESSINCSAGDMLLLWGRL TAPHCOQVIYWESESSQAEMEPSEGFLKAQASLRCQYWTLQSWVPEMQDPQSWKGKEGT 058 961 1118 1021 1060 1238 1119 1298 1358 g g ò g g ò g ò à 8 ઠે

AAO16619 standard; protein; 1378 AA016619; AAO16619 ID AAO1

RESULT

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(first

15-MAY-2003

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Human von Willebrand factor (vWF)-cleaving enzyme-related protein Human, protease inhibitor; gene therapy, vWF-cleaving enzyme; von Wilabyrand factor-cleaving enzyme; thrombocyropanic purpura; mycoavial infarction; oerebral infarction; attentoelesses

stenosis. platelet thrombosis; sapiens

WO200288366-A1.

07-NOV-2002

2001JP-00128342. 2001JP-00227510. 2001JP-00302977. 25-APR-2002; 2002WO-JP004141. 25-APR-2001; 27-JUL-2001; 28-SEP-2001;

Нататоро ú Nozaki KAGA) CHEMO-SERO-THERAPEUTIC RES INST Ή, Maeda Mimura N, WPI: 2003-120479/11. Soejima K,

2002JP-00017596

25-JAN-2002;

Nakagaki

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von Willebrand factor-cleaving enzyme, applicable in digmosis of, and supplementary therapsy for, thrombocit, thrombocytopento purpura, and for developing drugs for e.g. myocardial infarction and corebra infarction. N-PSDB: ABT32585.

The givening comprises the mains edit and coding sequence of a von Nullbarned fescor (VMF) -cleaving enzyme. The ONA and procein measurement to the internation are useful in the disapposit and researcher of the internation of the company of the c Sequence 1378 AA;

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Ouery Match 88.5%; Score 6661.5; DB 6; Length 1379; Best Local Similarity 92.6%; Peredi. No. 0; Matches 1779; Conservative 4; Mismatches 33; Indels 65; Matches 1779; Conservative 4; Mismatches 33; Indels 65;

157 9 AAGGILHLELLVAVGPDVFQAHQEDTBRYVLTNLNIGAELLRDPSLGAQFRVHLVKWVIL AAGGILHLELLVAVGPDVFQAHQEDTBRYVLTNLNIGAELLRDPSLGAQFRVHLVXVVIL Gaps 98

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TEPEGAPNITANLISSLLSVCGWSQTINPEDDIDPGHADLVLYITRFDLELPDGNRQVRG TEPEGAPNITANLISSLISVCGWSQTINPEDDIDPGHADLVLYITRFDLELPDGNRQVRG VIQLGGACSPINSCLITEDIGFDLGVIIAHEIGHSFGLEHDGAPGSGCGPSGHVMASDGA VIQLGGACSPTWSCLITEDTGFDLGVTLAHEIGHSFGLEHDGAPGSGCGPSGHVMASDGA -RARCVWDPPR APRAGLAWSPCSRROLLSLLSAG-28 61 218 278

APRAGLAMS POSRROLLS LIRTGALRYGPAAASTRYRGAPAGCAAMPLLORORAVPRGLR POPGSAGHPPDAOPGLYYSANEQCRVAP-GPKAVACTPAREHLDMCQALSCHTDPLDQSS

PQ-GCRLHLRQGAPG--ESAGGGLGLAVRSIRITQLTSPQTCMDMCQALSCHTDPLDQSS 247

CSRLLVPLLDGTECGVEKWCSKGRCRSLVELTPIAAVHGRWSSWGPRSPCSRSCGGGVVT CSRLLVPLLDGTECGVEKWCSKGRCRSLVELTPIAAVHGRWSSWGPRSPCSRSCGGGVVT 370 863

RRROCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLEFMSQQCARTDGQPLRSSPGGAS RRRQCNNPRPAFGGRACVGADI.QAEMCNTQACEKTQLEFMSQQCARTDGQPLRSSPGGAS 130

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FYHWGAAVPHSOGDALCRHXCRAIGESPIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGS PYHWGAAVPHSQGDALCRHMCRAIGESPIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGS CRIFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRARBYVTFLTVTPNLTSVYIA 190 118 550

699 729 657 789

GPLOEDADIOVYRRYGEEYGNLTRPDITFTYPOPKPROAWWAAVRGPCSVSCGAGLRWV NYSCLDQARKELVETVQCQGSQQPPAMPEACVLEPCPPYWAVGDFGPCSASCGGGLRERP GPLOEDADIQVYRRYGEBYGNLTRPDITFTYFOPKPROAWVWAAVRGPCSVSCGAGLRWV 969 220 330

VRCVEAGGSLLKTLPPARCRAGAQQPAVALETCNPOPCPARWEVSEPSSCTSAGGAGLAL ENETCVPGADGLEAPVTEGPGGVDEKLPAPEPCVGMSCPPGWGHLDATSAGEKAPSPNGS 558 NYSCLDQARKELVETVQCQGSQQPPAWPEACVLSPCPPYWAVGDFGPCSASCGGGLRERP VRCVENQGSLLKTLPPARCRAGAQQPAVALETCNPQPCPARWEVSEPSSCTSAGGAGLAL 718 350 990

849

777

Scelima K. 696 RNETCVPGADGLEAPVTEGPGSVDEKLPAPEPCVGMSCPPGWGHLDATSAGEKAPSPWGS INTGAQAAHVWIPAAGSCSVSCGRGLMELRFLCMDSALRVPVQRELCGLASKPGSRREVC

IRTGAQAAHVWTPAAGSCSVSCGRÖLMELRFLCMDSALRVPVQEELCGLASKPGSRREVC 897

778

1295 1257 1149 1179 1235 1355 957 1138 VQSSACGROHLEPTGTIDMRGFQQADCAVAIGRPLGEVVTLRVLESSLMCSAGDMLLLMG 1198 RLIWRKMCRKLLDWIFSSKINTLVVRQRCGRPGGGVLLRYGSQLAPETFYRECDMQLFGP 1296 WGEIVSPSLSPATSNAGGCRLFINVAPHARIAIHALATWWGAGTEGANASYILIRDTHSL 1258 WGEIVSPSLSPATSNAGGCRLFINVAPHARIAIHALATWMGAGTBGANASYILIRDTHSL 1356 RITARHGÇQVLYWESESSQAEMEFSEGFLKAQASLRGQYWTLQSWVPEMQDPQSWKGKEG 318 RITAPHGOOVLYWESESSOAEMEFSEGFLKAQASLRGOYWILQSWVPEMQDPGSWKGXEG QAVPCPARWQYKLAACSVSCGRGVVRRILYCARAHGEDDGEEILLDTQCQGLPRPEPQEA QAVPCPARWQYKLAACSVSCGRGVVRILYCARAHGEDDGEEILLDTQCQGLPRPEPQEA CSLEPCPPRWKVMSLGPCSASCGLGTARRSVACVQLDQGQDVEVDEAACAALVRPEASVP CLIADCTYRWHVGTWMECSVSCGDGIQRRRDTCLGPQAQAPVPADFCQHLPKPVTVRGCW CLIADCTYRWHVGTWMECSVSCGDGIORRRDTCLGPQAQAPVPADFCQMLPKPVTVRGCW AGPCVGOGTPSLVPHEEAAAPGRITATPAGASLEWSQARGLLFSPAFQPRRLLPGPQENS 1180 ----ACGROHLEPTGTIDMRGFQQADCAVAIGRPLGEVVTLRVLESSLNCSAGDMLLLWG RLTWRKOMCRKILLDMIFSSKINTLVVRQRCGRPGGGVILLRYGSQLAPBIFYRBCDMQLFGP CSLEPCPPRWKVMSLGPCSASCGLGTARRSVACVQLDQGQDVZVDBAACAAL AGPCVGQGTPSLVPHERAAPGRTTATPAG-------T 1416 T 1378 1378 970 868 030 1090 1150 1078 1236 1416 g 유 a g à g ò 음 ò 음 à

> 21.7 120 180 310 240 297

AA016620 standard; protein; 1323 AA AA016620 AAC16620 ID AAC1

RESULT

357 417 549 423

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(first entry

15-MAY-2003

Human von Willebrand factor (vWF)-cleaving enzyme-related protein

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Human; protease inhibitor; gene therapy; vWP-cleaving enzyme; von Wilsbrand factor-cleaving enzyme; thrombocytopenic purpura, myocardial infarction; cerebral infarction; arteriosclerosis; blacelet thrombosis; stenosis. Homo sapiens

25-APR-2002; 2002WO-JP004141 40200288366-A1 07-NOV-2002

Nozaki C, (KAGA) CHEMO-SERO-THERAPEUTIC RES INST Maeda H, 25-APR-2001, 2001JP-00128342. 27-JUL-2001, 2001JP-00227510. 28-SEP-2001, 2001JP-00302977. 25-JAN-2002, 2002JP-00017596 Mimure N,

Hamamoto T. WPI: 2003-120479/11.

Nakadaki

N-PSDB; ABT32586

1089

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1176 GVILRYGSGLAPETFYRECDMQLFGPWGEIVSPSLSPATSNAGGCRLFINVAPHARIAIH 1235
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                                                                                           IRTGAQAAHVWTPAAGSCSVSCGRGLMELRFLCMDSALRVPVQEELCGLASKPGSRREVC
                                                                                                                                                                                                                                                                      QAVPCPARMQYKLAACSVSCGRGVVRRILYCARAHGEDDGBEILLDTQCQGLPRPEPQEA
                                                                                                                                                                                                                                                                                                                             CSLEPCPPRWKVMSLGPCSASCGLGTARRSVACVQLDQGQDVEVDEAACAALVRPEASVP
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RNETCVPGADGLEAPVTEGPGSVDEKLPAPEPCVGMSCPFGMGHLDATSAGEKAPSPWGS
                                                                                                                                            IRTGAQAAHVWTPAAGSCSVSCGRGLMELRFLCMDSALRVPVQEELCGLASKPGSRREVC
                                                                                                                                                                                                         QAVPCPARWQYKLAACSVSCGRGVVRRILYCARAHGEDDGEEILLDTQCQGLPRPEPQEA
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2001US-0307393P.
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25-JUL-2001;
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      von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and
supplementary therapy for, thrombotic thrombosytopenic purpura, and for
developing drugs for e.g. wycasidial inferction and cerebral inferction
                                                                                                                                                                          The invention comprises the maino acid and coding sequence of a von 
the landermal factor (WRF)-clasving ensyme. The DNA and procise sequences the invention are useful, in the diagnosis and treatment of 
the invention are useful, in the diagnosis and treatment of 
the invention are useful, in the diagnosis and treatment of 
infarction, esembral infarction, are residenteres, placelet thrombosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGILHLELLVAVGPDVFQAHQEDTERYVLTNINIGAELLRDPSLGAQFRVHLVKMVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGGILHLBLLVAVGPDVFQAHQEDTERYVLTNINIGAELLRDPSLGAQFRVHLVRWVIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VIQLGGACSPIWSCLITEDIGFDLGVIIAHEIGHSFGLEHDGAPGSGCGPSGHVWASDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APRAGLAWSPCSRRQLLSLLSAG------RARCVWDPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 APRAGLAWSPCSRRQLLSLLRTGALRVGPAAASTRVRGAPAGCAAWPLLQRQRAVPRGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POPGSAGHPPDAQPGLYYSANEQCRVAF-GPKAVACTFAREHLDMCQALSCHTDPLDQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 PQ-GCRLHLRQGAPG--ESAGGGLGLAVRSLRITQLTSPQTCMDMCQALSCHTDPLDQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSRLLVPLLDGTECGVEXWCSKGRCRSLVELTPIAAVHGRWSSWGPRSPCSRSCGGGVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSRLLVPLLDGTECGVEKWCSKGRCRSLVELTPIAAVHGRWSSWGPRSPCSRSCGGGVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-5 REBCONNERPARGERACYGADLOAEMCNTCACEKTOLEFMSCOCARTDGOPLRSSPGGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYHWGAAVPHSQGDALCRHMCRAIGESPIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 FYHWGAAVPHSONDALCRIPCRAIGESFINKRODSFLDGTRCMPSGPREDGTLSLCVSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.1 Gaps
                                                                                                                                                                                                                                                                                                                                   l stenosis. The present amino acid sequence represents a human von
lebrand factor (vWF)-cleaving enzyme-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 1323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.1%; Score 6752.5;
93.3%; Pred. No. 0;
11ve 4; Mismatches
                                                                                                                         Claim 4; Page 112-121; 144pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.1
Best Local Similarity 93.3
Matches 1257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1323 AA;
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us-09-836-712-2.rag

669 759

540 LPRLEBIRIWGPLQEDADIQCVKKQIPGSSAYSLNQDFPVLGLRNRTVINTGLRHWPDVG 00 IEGAAQPVSCALCYPQSLVQVYRRYGEBYGNLTRPDITFITFOPKFRQAWTWAAVRGFCS

-----QVYRRYGBEYGNLTRDITTYRQPKPRQAWWAAVRGPCS

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                                                                                                                            New purified human ADM-TS-like protein, useful for identifying doublators of protein arthrity for treating cardiovascular or liver disorder or chronic obstructive pulmonary disease.
                                                                                                                                                                                                                                                                                                                           Claim 25; Fig 2; 106pp; English
2002-383274/41
WPI; 2002-383274,
N-PSDB; ABK49356
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Sequence 933 AA;

Gaps 65; DB 5; Length 933; Inde18 9; 57.2%; Score 4434.5; 91.6%; Pred. No. 0; ive 2; Mismatches 819, Conservative Local Similarity Query Match Matches Best

113 OEDTERYVLTNINIGAELIRDPSLGAQFRVHLVKKVILLTEPEGAFNITANLTSSLLSVCG 179 159 66 .00 QEDTERYVLTNINIGAELLRDPSLGAQFRVHLVKAVILTEPEGAPNITANLISSLLSVCG 64 LEP----QAVSSYLSPGAPLKGRPPSPGFQRQRQRRAAGGILHLELLVAVGPDVFQAH 41 LEPWCSLKRTIALCSPSPP-PGRPPSPGPQRQRQRRAAGGILHLELLVAVGPDVFQAH 120 g ò

DIGVTIAHEIGHSFOLEHDGAFGSOCGFSGHVMASDGAAPRAGLAWSFCSRROLLSLLSA 299 80 WSQTINPEDDTDPGHADLVLYITRPDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGP 160 WSQTINPEDDTDPGHADLVLYITRPDLELPDGNRQVRGVTQLGGACSPTWSCLITEDIGF 240

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239

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GTLSICVSGSCRTFGCDGRMDSOQVMDRCQVCGGDNSTCSFRKGSFTAGRAREYVTFLTV TPNLTS VYIANHRPLFTHLAVRIGGRYVVAGKONSISPNTTYPSLLEDGRVEYRVALTEDR TPNLTSVYIANHRPLFTHLAVRIGGRYVVAGKMSISPNTTYPSLLEDGRVEYRVALTEDR

9

LPRLEBIRIWGPLOSDADI --

629 639

760 VSCGAGLERWYNYSCLDDARKELVETVQCQGSQQPPAWPEACVLEPCPPYWAVGDFGPCSA 819 820 SCGGGLRERPURCVEAGGSLLKTLPPARCRAGAQQBAVALETCNPQPCPARWEVSEPSSC 879 SCGGGLRERPVRCVEAOGSLLKTLPPARCRAGAOOPAVALETCNPOPCPARWEVSEPSSC 839 20 VSCGAGLRWVNYSCLDQARKELVETVQCQGSQQPPANPEACVLEPCPPYMAVGDFGPCSA 840 ISAGGAGIALENETCVPGADGLEAPVTEGPGSVDEKLPAPEPCVGMSCPPGWGH 893 880 TSAGGAGLALENZICVPGADGLEAPVIEGPGSVDEKLPAPERPCVGMSCPPGWGH ò 8 à 유 ò 쉼

entreellilist marix Ainestin nursitation suppliesting agents mattraction immunologic recognition; gastrointestinal irradistion; chemothesspy; proteologis; apoptosis; adints, anti-angiogenic, intestinal polypeptide; wound healing Amino acid sequence of a human zdint5 polypeptide AAG63829 standard; protein, 1120 AA (first entry) 29-OCT-2001 AAG63829;

AAG63829 ID AAG6

Location/Qualifiers Homo sapiens

/notes "potential N-linked glycosylation site" 176 /note= "potential N-linked glycosylation site" 533 /note= "potential N-linked glycosylation site" 560 /note= "potential N-linked glycosylation site" "potential N-linked glycosylation site' 'note= "unspecified residue encoded by TTN" /note= "potential N-linked glycosylation "potential N-linked glycosylation /note= 7 note= 485 Wisc-difference Modified-site Modified-site Modified-site Additied-site Addified-site Addified-site Modified-site

39-FEB-2001, 2001WO-US004198 .O-FEB-2000; 2000US-00501806 16-AUG-2001

40200159112-A1

Holloway JL, Sheppard PO WPI; 2001-522477/57

ZYMO) ZYMOGENETICS

N-PSDB; AAH74765

New anti-anglogenic intestinal polypeptides, zdint5 polypeptides, which are merbers of disintegrin proteases, for modulating extracellular matrix interaction, tunor suppression and wound healing.

Claim 2, Page 84-88; 92pp; English

The present sequence represents a human catter polympride . The dather the catters of the constraint of the catter and the cat

CVKKQIPGS----SAYSLN 625

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550 EYVTFLTVTPNLTSVYIANHRPLFTHLAVRIGGRYVVAGKAKISPNTTYPSLLEDGRVZY

Sequence 1120 AA:

immunology, trauma and epithelial disorders

45.8%; Score 3553.5; DB 4; Length 1120; 54.2%; Pred. No. 2.9e-258; sive 21; Mismatches 108; Indels 517; Gaps 766; Conservative Query Match Best Local Similarity Matches 766; Conserval

793 BVDEAACAALVAAR 807 -----TAPTAGM-----LAPGWR

67

68 AVSSYLSPGAPLKGRPPSPGFQRQRQRRAAGGILHLELLVAVGPDVFQAHQEDTERYV 127 8 KAPSHSAPLIGLALLRMHQRHPRARCPPLCVAGILAGFLIGCWGPSHFQGSCLQALSPQ 15 KAPSHSAPLLGLALLRMHQRHPRARCPPLCVAGILACGFLLGCWGPSHFQQSCLQALBPQ 75 AVSSYLSPGAPLKGRPPSPGFQRQRQRQRRAAGSILHLELLVAVGPDVFQAHQEDTERYV

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28 LINLNIGABLIRDPSLGAGFRVHLVKAVILTEPEGAPNITANLTSSLLSVCGWSQTINPE 135 LINLNIGABLIRDPSIGAQFRVHLVKWVILTEPQGAPNITANLISSLLSVCGWSQTINPE

g

DDTDPGHADLVLYITRFDLELPDGRRQVRGVTQLGGACSPTWSCLITBDTGFDLGVTIAH 247 DDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAH 88

254 314 359 363 419 405 472 455 531 489 591

311 AGGCRLFINVAPHARIAIHALATNWGAGTEGANASYILJRDTHSLRTTAFH-GQQVLYWE 1369

865 PSSKTNTLV

----SIPCRFLGDMLLLWGRLTWRKMCRKLLDMT

829 RGSAGP----

134 187 194

24

874 ----IRDTHSLRTTAPHRAAGALTGS 895

1370 SESSOAEMBFSEGFLKAQASLRGQYWTLQSWV 1401 ORAARLRMEFSEGFLKAQASLRGCYWTLCSWL 927

EIGHSFGLEHDGAPGSGCGPSGHVWASDGAAPRAGLAWSPCSRRQLLS----LLSAGRAR 303 255 BIGHSFGLEHDGAPGSGCGPSGHVMASDGAAPRAGLAWSPCSRRGLLSAGPGALRVGTRR 304 CVWDPPRPQPGSAGHPPDAQP-GLYYSANEQCRVAFGPKAVACTFAREHLDM---CQALS 248

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3.5 GL-----KPGFRGAPAGWRSLGLYYSANEQCHVAPGPPG-----CRLHIRQGAPCQALS CHIDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRCRSLVELTPIAAVHGRWSSWGPRSPC 960

CHTDPLDOSSCSRLLVPLLDGTECGVEK-----VHGRWSSWGPRSPC SRSCGGGVVTRRRQCNN-----PRPAFGGRACVGADLQAEMCNTQACEKTQLEFMSQQ 106 SRSCGG-----CGHQEAAVQOPQVPCGGLFCQGMKLGGGWGTCPSCSVQDTLFHS--364 50

190 MPSGPREDGTLSLCVSGSCRVRGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAR 549 CARTDGQPLRSSPGGASPYHWGAAVPHSQGDALCRHMCRAIGESFIMKRGD-SFLDGTRC -----ALP---GDALCRHMCRAIGESXHHBAWETASSNGTRC 532 MPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAR 173 156

EYVTFLTVTPNLISVYIANHRPLFTHLAVRIGGRYVVAGKMSISPNTTYPSLLEDGRVEY 651

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zdints; ADAM; a disintegrin and metalloprotease; detergent home defence: tumour; extracellular matrix repair; proteclysis; approxeis, axerigenesis; baterial infection; Confu's disease; inflammatory bowel disease; food poisoning; melanom; dedemnerative disease; chronosome 9434; wound healing; TSP-1; firromopoundin domain. ABG74113 standard, protein, 1120 (first entry) Human mature zdints. 01-MAY-2003 ABG74113; Human) RESULT 12 ABG74113 2525555555555555

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'note= "Encoded by CTGTGAAAT" /notes "Encoded by TTN" Location/Qualifiers /label= Misc-difference 1118 Misc-difference

JS2002142439-A1 03-OCT-2002.

10-PEB-2000; 2000US-0181511P 09-FEB-2001; 2001US-00781080

(HOLL/) HOLLOWAY J L. (SHEP/) SHEPPARD P O. (YAMA/) YAMAMOTO G.

Holloway JL, Sheppard PO, Yamamoto G; N-PSDB, ABX15947, ABX15948. WPI; 2003-174136/17

New zdinck polypepidea, useful jor diagnoning, prewanting or treating proceeding preventing or treating proceeding proceeding or proceeding pro

Claim 2, Page 32-34; 37pp; English.

and situation to the total the control to distinct the control of an entilliprocesses (AAAN), the speak for which is located on human straight and setal interesting the control of the co

Sequence 1120 AA

Indels 517; Gaps Query Match 45.8; Score 3553.5; DB 6; Length 1120; Best Local Similarity 54.28; Pred. No. 2.96-258; Masche Strone Strone

8 KAPSHSAPLIGLALLEMHQRUPRARCPPLCVAGILACGFLLGCWGPSHFQQSCLQALEPQ

1072 BVDEAACAALVRPEASVPCLIADCTYRWHVGTWMECSVSCGDGIQRRRDTCLGFQAQAPV 1131

793 EVDEAACAALVAAR---

135 LTNINIGABLIRDFSLGAOFRVHLVAMVILTBPQGAPNITANLTSSLLSVCGWSCTINPE 194 DDTDPGHADLVLYITRPDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAH 247 DOTOPGHADLVLYITRPDLBLPDGNRQVRGVTQLGGAC8PTW8CLITBDTGFDLGVTIAH 254 248 EIGHSFGLEHDGAPGSCCGPSGHVMASDGAAPRAGLAWSPCSRRQLLS----LLSAGRAR 303 CVWDPPRPQPGSAGHPPDAQP-GLYYSANEQCRVAFGPKAVACTFAREHLDM---CQALS 359 GL-----KPGFRGAPAGWRSIGLYYSANBQCHVAFGPFG-----CRIHIRQGAPCQALS 363 360 CHIDPIDQSSCSRLLVPLLDGIECGVEKWCSKGRCRSLVELTPIAAVHGRWSSWGPRSPC 419 364 CHIDPLDQSSCSRLLVPLLDGTECGVEK------VHGRWSSWGPRSPC 405 420 SRSCGGGVVTRRROCHN-----PRPAPGGRACVGADLQAEMCNTQACEKTQLEFMSQQ 472 406 SRSCGG-----CGHQERAVQQPQVPQGGLFCQGMKLGGGWGTCPSCSVQDTLFHS-- 455 473 CARTDGQPLRSSPGGASPYHWGAAVPHSQGDALCRHMCRAIGESPIMKRGD-SFLDGTRC 531 456 ------ADALCRHMCRAIGESXHHEAWETASSNGTRC 489 190 MPSGPREDGTLSLCVSGBCRVRGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGBFTAGRAR 549 550 EYVTELTVTPNLTSVYIANHRPLFTHLAVRIGGRYVVAGKMSISPNTTYPSLLEDGRVEY 609 552 RVALTEDRIPRIEEIRIMGPLQEDADIQVYRRYGEEYGNLTRPDITFTYFQPKPRQAWVW 711 609 712 AAVRGPCSVSCGAGLRWYNYSCLDQARKELVETVQCQGSQQPPAMPEACVLEPCPPYMAV 771 \$10 -----SDAKKÖIPGS-----SDAKKIN 625 772 GDFGPCSASCGGGLRERPVRCVZAQGSLLKTLPPARCRAGAQQPAVALETCNPQPCPARW 831 26 ODPPVL-----GLRNRTV------HW 646 332 EVBEPSSCTSAGGAGLALENETCVPGADGLEAPVTEGPGSVDEKLPAPEPCVGMSCPPGW 891 653 ----GAGLMELRFLCMDSALRVPV 672 673 QEBLOGLASKPGSRREVCQAVPCPARWQYKLAACSVSCGRGVVRRILYCARAHGEDDGEE 732 133 ILLDIGCOGLPRPEPQEACSLEPCPPRWKVMSLGPCSASCGLGTARRSVACVQLDQGQDV 792 AVSSYLSPGAPLKGRPPSPGPGRQRQRQRRAAGGILHLELLVAVGPDVPGAHQEDTERYV 127 75 AVSSYLSPGAPLKGRPPSPGPGRQRQRQRRAAGGILHLELLVAVGPDVPQAHQEDTERYV 134 128 LTNLNIGAELLRDPSLGAOPRVHLVKWYILTEPEGAPNITANLTSSLLSVCGWSQTINPE 187 255 EIGHSFGLEHDGAPGSGCGPSGHVMASDGAAPRAGLAWSPCSRRQLLSAGPGALRVGTRR 314 532 MPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAR 592 EYVIPLIVIPNLISVYIANHRPLFTHLAVRIGGRYVVAGKMSISPNTIYPSLLEDGRVEY 647 -----PDVGIE----992 GHLDATSAGEKAPSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGLMELRFLCNDSALRVPV 952 QEBLCGLASKPGSRREVCQAVPCPARMQYKLAACSVSCGRGVVRRILYCARAHGEDDGEE 012 ILLDIGCOGLPRPEPQBACSLEPCPPRWKVMSLGPCSASCGLGTARRSVACVQLDQGQDV KAPSHSAPILGLALLRMHQRHPRARCPPLCVAGILACGFLLGCWGPSHFQQSCLQALEPQ 188 용 a a ò 용 ò 용 è 쉺 ò 용 õ 용 à 윤 Š 8 ò g à a ò 셤 ò g g 6 ò ò

1250 PSSKTNTLVVRQRCGRPGGGVLLRYGSQLAPETFYRECDMQLFGPWGEIVSPSLSPATSN 1310 133 PADFCQHLPKPVTVRGCWAGPCVGQGTPSLVPHBEAAAPGRTTATPAGACGRQHLBFTGT 1191 828 864 873 -----GOLSPVSLP-----TAPTAGM-----LAPGWR 1192 IDMRGPGOADCAVAIGRPLGEVVTLRVLBSSINCS-AGDMLLMGRLTWRKKYCRKLLDMT 8.29 RGSAGF------SLPCRFLGDMLLLWGRLTWRRCKLLDMT 865 PSSKTNTLV-----1251 염 à ò

1311 AGGCRLFINVAPHARIAIHALATNWGAGTEGANASYILIRDTHSLRTTAFH-GQQVLYWE 1369 IRDIHSIRITARHRAAGALIGS 895

1370 SESSOAEMEFSEGFLKAQASLRGQYWTLQSWV 1401

à

896 ORAARIRMEFSEGFIKAQASIRGOYWTIOSWI 927

RESULT 13 ABR961

ABR96171 Standard; protein; 984 AA

Human NOV17a protein SEQ ID NO:84.

15-SEP-2003 (first entry)

Human, NOY, O poceal-conded a respons, gyorestic patientowards in amunoappressive, marietty antiachments misserson conference and compensate and effects of the defendance of the state of the control of streaments cannot defent policeary familiary poetate connect accurate disease of the control of the control of the control of streaments cannot defent policeary familiary poetate connect control disease of the control of the control of the control of property of the control of the control of the control of the photogeneous supplies (connect defents).

Homo sapiens.

W0200290568-A2 14-NOV-2002. 32-MAY-2002; 2002WO-US014341

23-MAY-2001, 2001US-0293107P. 24-MAY-2001, 2001US-0293589P. 25-MAY-2001, 2001US-0293747P. 29-MAY-2001, 2001US-029410P. 2001US-0294434P. 2001US-0312192P. 2001US-0313173P. 2001US-0318728P 2001US-0335910P 12-SEP-2001;

28-NOV-2001, 2001US-033891P. 28-NOV-2001, 2001US-0333942P. 03-JAN-2002, 2002US-0345776P. 04-JAN-2002, 2002US-0345220P. 01-MAY-2002, 2002US-00136071.

CURA-) CURAGEN CORP.

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WPI; 2003-111987/10. N-PSDB, ACP16980

New WOVY polypaptides and polymuclectides useful for treating or preventing e.g. cardiosypathy, atherosclarosis hypertension, congenital hear defects, acris series acras septal defect, or attiowentricular canal defect.

Claim 1, Page 173; 491pp; English.

Processes to Activation encode the human openic-coupled exception (OCCE)
processes designated NOW processes with ARREAD to ARREAD. The
NOW sequences can have opposited, called an arread to the control of the coupled of the coupled

Sequence 984 AA;

Gaps 29; Mismatches 108; Indels 256; 30.2%; Score 2340; DB 6; Length 984; 56.0%; Pred. No. 6.6e-167; 500; Conservative Best Local Similarity Matches 500; Conserv Ouery Match

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419 360 GVTOLOGACSPTWSCLITEDTGFDLGVTIAHEIGHRYVAPPAVPRIWOGADLGTQGGGL 217 GVTQLGGACSPTWSCLITEDIGFDLGVTIAHEIGH------

420 SKOWULVEFLORSLYPSPROTOVSFOLEHDGAPGSGCGPSGHVMASDGAAPRAGLAMSPC 479 252 -----SPGLEHDGAPGGCGPSGHVMASDGAPRAGLAWSPC

289 SRRQLLSLLSAGRARCVWDPPRPQPGSAGFPPDAQPGLYYSANBQCRVAFGPKAVACTFA 348

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLEFMSQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532 MPSGPREDGTLSLCVSGSCRIFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAR 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 MPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCSFRKGSFTAGRAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   592 RYVTFLTVTPNLTSVYIANHRPLFTHLAVRIGGRYVVAGMASISPNTTYPSLLEDGRVEY 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 BYVTPLTVTPNLTSVYIANHRPLFTHLAVRIGGRYVVAGKASISPNTTYPSLLEDGRVEY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuroprotective; immunomodulator; cancer; chromosome 9p34; cytostatic;
the complex complex complex complex complement; wound; burn;
aloer; Alzieiner; a disease; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEXWCSKGRCRSLVELTPIAAVHGRWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 QCARTDGQPLRSSPGGASFYHWGAAVPHSQGDALCRHMCRAIGESFIMKRGDSFLDGTRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 OCARTOGOPLESSPEGASFYHWGAAVPHSCGDALCRHMCRAIGESFIMKRGDSFLDCTRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 LDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEXKCSKGRCRSLVELTPIAAVHGRWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               imyotrophic lateral sclerosis; autoimmune disorder; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                652 RVALTEDRIPRIBEIRIWGPLQEDADIQV 680
Disclosure, Page 37-38, 41pp; English
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Best Local Similarity 99.71
Matches 328; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 364 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             906
       180 SRRQLLSLL--GRARCVWDPPRPQPGSAGHPPDAQPGLYYSANEQCRVAFGPKAVAC--- 534
                                                                      408
                                                                                                                                            535 ----DMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRCRSLVELTPIAAVHG 590
                                                                                                                                                                                                            468
                                                                                                                                                                                                                                                                                                                                                                                                                521 -----YRREGAFLSGCPGGK-----PEVSHSQLFRASSVHACKLGSVLSDVHQCRHMCR 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.1.2 AIGESFIMKRODSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVC 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        570 AIGESPIMKREDSFIDGTRCMPSGPREDGTLSLCVSGSCRVGGCDGRMDSQQVMDRCQVC 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572 GGDNSTC-----GRARENTELT 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     730 GGDNSTCHGVEGPRSHQDPGTPETSPPGRATAPILPAGPRQACGTGGWAASRGQVRNVT 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           599 VIPNLISVYIANHRPLFIHLAVRIGGRYVVAGKAKIISPNITYPSILLEDGRVEYRVALIED 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 790 TSP-----IPARPICLOLPASVGQRGPQRAVGGRARATSLNS-----IPD 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 559 RLPRLEBIRINGPLQEDADI---QVYRRYGERYGNLT-RPD--ITPTYPQPKPRQAWVWA 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       834 SLPSTTQ----GGPQMAHSSAISSSLHRGHWGYQGMVTWSPNHLVVASARIPKPRQAWVWA 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel purified aggrecanase polypeptide useful for developing inhibitors and antibodies to the aggrecanase polypeptide. Wich are useful for treating aggrecanase associated condition such as osteosrthritis.
                                                                             349 REHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEXWCSKGRCRSLVBLTPIAAVHG
                                                                                                                                                                                                                                                                                  591 RWSSWGPRSPCSRSCGGGV/TRRRQCNNPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVRGPCSVSCGAGETW
                                                                                                                                                                                                            109 RWSSWGPRSPCSRSCGGGUV/TRRROCNNPRPAFGGRACVGADLOAEMCNTOACEKTOLEF
                                                                                                                                                                                                                                                                                                                                                 169 MSQQCARTDGQPLRSSPGGASFYHWGAAVPHSQ------GDAL----CRHMCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aggrecanase; osteopathic; antiarthritic; antiinflammatory; human;
cartilage; osteoarthritis; inflammatory disease; enzyme; HsaOll374,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            773 DFGPCSASCGGGLRERPVRCVEAGGSLLKTLPPARCRAGAQQPAVALETCNPQ 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    907 -----GRIIHSTACVEAGGSLLKTLPPARCRAGAQOPAVALETCNSE 948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agostino MJ, Wolfman NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU97642 standard; protein; 364 AA
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Yang Y, Wehrman T, Drmanac RT;
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412 SWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACBKTQLEFMSQ

1 MDMCQALSCHIDPLDQSSCSRLLVPLLDGTECGVEKMCSKGRCRSLVELTPIAAVHGRWS 60

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Search completed: March 13, 2004, 07:39:00 Job time : 216,238 secs

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TITLE OF INVENTION: Aggrecanase Molecules
FILE REFERENCE: 08702.0073
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CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: 60/241,469
PRIOR FILING DATE: 2000-10-18
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Publication No. US20030105313A1
GENERAL INPORMATION:
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Local Similarity 97.5%;
nee 1392; Conservative
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APPLICAM: SHEPRAD, DAUL
APPLICAM: YAMADOO, GAYLE
TITLE OF IMPRICOR: ALL -Angiogenic Intestinal Peptides,
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CURBENT APPLICATION NUMBER: US/09/781,080B
CURBENT FILING DESTE: 2002-01-30
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Patent No. US20020142439A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .44 GAQFRVHLVKMVILTEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDFGHADLVLYITR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 FDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPGS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 NAGGCRLFINVAPHARIAIHALATNWGAGTEGANASYILIRDTHSLRTTAFHGQQVLYWE
                                                              ACSVSCGRGVVRRILYCARAHGEDDGEEILLDTQCQGLPRPEPQEACSLEPCPPRWKVMS
                                                                                                                                               961 ACSVSCGRGVVRRILYCARAHGEDDGEEILLDTOCOGLPRPEPOEACSLEPCPPRWKVMS
                                                                                                                                                                                                                                         igposasogigtarrsvacvoldogodvevdbaacaalvrpeasypciiadotyrwhygt
                                                                                                                                                                                                                                                                                                                 LGPCSASCGLGTARRSVACVQLDQGQDVEVDEAACAALVRPEASVPCLIADCTYRMHVGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1141 HEEAAAPGRITATPAGASLEWSQARGLLFSPAPQPRRILPGPQENSVQSSACGRQHLEPT
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46.6%; Score 3609.5; DB 14; Length 842;
Best Local Similarity 77.1%; Pred. No. 2.5e-257; Indels 101; Gaps
Matches 712; Conservative 20; Mismatches 90; Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1370 SESSOARMEPSECFLKACASLRGCYWTLCSWVPEMODPCSWKGKEGT 1416
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ORGANISM: Homo sapiens
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1251 FSSKTWTLVVRQRCGREGGGVLLRYGSQLAPETFYRRCDMQLFGFWGETVSPSLSPATSN 1310 1311 AGGCRLFINVAPHARIAIHALAINMGAGTEGANASYILIRDIHSLRTIAFH-GGGVLYWE 1369 012 ILLDIQCOGLPRPEPQEACSLEPCPPRWKYMSLGPCSASCGLGTARRSVACVQLDQGQDV 1071 EVDERACALURPEASUPCLIADCTYRWHVGTWMECSVSCGDGIQRRRDTCLGPQAQAPV 1131 132 PADFCQHLPKPVTVRGCWAGPCVGQGTPSLVPHBBAAAPGRTTATPAGACGRQHLBPTGT 1191 1192 IDMRGPGQADCAVAIGRPLGBVVTLRVLESSLNCS-AGDMLLLWGRLTWRKMCRKLLDWT 1250 733 ILLDIQCQGLPRPEPQEACSLEPCPPRWKVMSLGPCSASCGLGTARRSVACVQLDQGODV 792 793 EVDEAACALVAAR GOLSPVSLP----TAPTAGM----LAPGWR 828 829 RGSAGP----SLPCRFLGDMLLLWGRLTWRKMCRKLLDWT 864 865 FSSKTNTLV 874 ----IRDIRITAFHRANGALIGS 895 Version #1,30 ADDRESSEE: American Home Products Corporation APPLICANT: Recie, Lise, A.
APPLICANT: Recie, Lise, A.
APPLICANT: Recie, Medies, J.
Wolfens, Nell, Stabbeth
TYLE OF WOTTISE, Blisdbeth
TYMERE OF SENDINCES: 6 CORRESPONDENCES: 6 CORRESPONDENCES: 6 CORRESPONDENCES: 6 CORRESPONDENCES: 6 CORRESPONDENCES: 6 CORRESPONDENCES ADDRESS: 6 CORRESPONDEN 1370 SESSQAEMEFSEGFLKAQASLRGGYWTLQSWV 1401 896 ORAARLRMEFSEGFLKAOASLRGOYWTLOSWL 927 PRICE APPLICATION DAYS.

PRILING DAYS. (1986)

FILLING DAYS. (APPROACH 1986)

ATTORNEY MARKET MARKET 12, 489

ROBERT PARTITUM NEW ARREST 12, 484

ROBERT PARTITUM NEW ROBERT 12, 481

REPRESENCE/DOCURT NEWERS 13, 445

FILLINGENCE: (1971), 660, 5606 COMPUTER RELACABLE TORN.

COMPUTER FIRST STORY AS A COMPUTER TO STORY AS A COMPUTER TO STORY AS A COMPUTER STORY AND STORY AS A COMPUTER STORY AS STREET: One Campus Drive FELBFAX: (973) 683-4117 LENGTH: 365 amino acids Sequence 5, Application US/09978979 Patent No. US20020151702A1 GENERAL INFORMATION: INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: CITY: Parsippany STATE: New Jersey COUNTRY: USA US-09-978-979-5 072 셤 952 QEBLCGLASKPGSRREVCQAVPCPARWQYKLAACSVSCGRGVVRRILYCARAHGEDDGEE 1011 550 EYVTFLTVTPNLTSVYIANHRPLFTHLAVRIGGRYVVAGKWGISPNTTYPSLLEDGRVEY 609 392 GHLDATSAGEKAPSPWGSIRTGAOAAHVWTPAAGSCSVSCGRGLMELRFLCMDSALRVPV 951 GAGLMELRFLCMDSALRVPV 672 248 BIGHSFGLEHDGAPGSGCGPSGHVMASDGAAPRAGLAWSPCSRRCLLS----LLSAGRAR 303 255 EIGHSFGLEHDGAPGSGCGPSGHVMASDGAAPRAGLAWSPCSRRGLLSAGPGALRVGTRR 314 304 CVWDPPRPQPGSAGHPPDAQP-GLYYSANEQCRVAFGPKAVACTFAREHLDM---CQALS 359 315 GL-----KPGFRGAPAGWRSLGLYYSANBQCHVAPGPPG-----CRLHLRQGAPCQALS 363 CHIDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRCRSLVELTPIAAVHGRMSSWGPRSPC 419 364 CHTDPLDQS8CSRLLVPLLDGTECGVEK------VHGRWSSWGPRSPC 405 120 SRSCGGGVVTRRRQCNN-----PRPAFGGRACVGADLQAEMCNTQACEKTQLEFMSQQ 472 106 SRSCGG-----CGHQEAAVQQPQVPQGGLFCQCMKLGGGWGTCPSCSVQDTLFHS-- 455 531 456 ------ALP---GDALCRHWCRAIGESXHHEAWETASSNGTRC 489 532 MPSGPREDGTLSLCVSGSCRIPGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAR 591 90 MPSGPREDGTLSLCVSGSCRVRGCDGRMDSQQVWDRCQVCGCDNSTCSPRKGSFTAGRAR 549 592 EYYTFLTVTPNLTSVYIANHRPLFTHLAVRIGGRYVVAGKMSISPNTYPSLLEDGRVEY 651 5.2 RVALTEDRIPERIRINGPLORDADIQVYRRYGERYGNITRPDITFTYFQPKPRQAWVW 711. 019 712 AAURGPCSVSCGAGLRWUNYSCLDQARKELVETVQCQGSQQPPAWPEACVLEPCPPYMAV 771 510 ------SPYSLN 625 772 GDFGPCSASCGGGLRERPVRCVEAGGSLLKTLPPARCRAGAGGPAVALETCNPQPCPARW 831 526 ODPPVL----GLRNRTV-----HW 646 332 BVSEPSSCTSAGGAGLALENETCVPGADGLEAPVTEGFGSVDEKLPAPEPCVGMSCPPGW 891 7.4 68 AVSSYLSPGAPLKGRPPSPGFQRQRQRQRRAAGGILHLELLVAVGPDVFQAHQEDTERYV 127 75 AVSSYLSPGAPLKGRPPSPGFQRQRQRRAAGGILHLELLVAVGPDVFQAHQEDTERYV 134 128 LTNLNIGAELLRDPSLGAQFRVHLVKMVILTEPEGAPNITANLISSLLSVCGWSQTINPE 187 135 LININIGAELLRDPSLGAGFRVHLVKMVILTEPQGAPNITANLTSSLLSVCGWSGTINPE 194 DDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAH 247 195 DDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAH 254 13 CARTDGODLRSSPGGASFYHWGAAVPHSOGDALCRHWCRAIGESFIMKRGD-SFLDGTRC Query Match Local Samilarity 54.58; Score 3553.5; DB 9; Length 1120; Best Local Samilarity 54.54; Pred. Nv. 56-52; Nv. 56-538 Matches 765; Conservative 21; Nismatches 108; Indels 517; Gaps 8 KAPSHSAPLLGLALLRMHQRHPRARCPPLCVAGILACGFLLGCWGPSHFQQSCLQALEPQ 15 KAPSHSAPLIGLALLRWHORHPRARCPPLCVAGILACGFLLGCWGPSHFOOSCLOALEPO , LOCATION: (1)...(1120)
, OTHER INFORMATION: Xaa = Any Amino Acid
US-09-781-0808-11 88 g a à a à ŝ å

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61 SWGPRSFCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQABMCNTQACEKTQLEFMSQ 120
                                                                              472 OCARTDGQPLRSSPGGASPYHWGAAVPHSQGDALCRHWCRAIGESFIMKRGDSFLDGTRC 531
                                                                                                                                    121 QCARTDGQPLRSSPGGASFYHWGAAVPHSQGDALCRHWCRAIGBSFIMKRGDSFLDGTRC 180
                                                                                                                                                                                                                           532 MPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAR 591
                                                                                                                                                                                                                                                                                                 181 MPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAR 240
                                                                                                                                                                                                                                                                                                                                                                               592 BYVTFLTVTPNLTSVYIANHRPLFTHLAVRIGGRYVVAGKKISPNTTVPSLLEDGRVEY 651
                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SYVTFLIVTPNLTSVYIANHRPLFTFLAVRIGGRYVVAGKASISBNTTYPSLLEDGRVEY 300
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COMPUTER: ISM PC compatible
OPPRATING SYTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Taccie, Lisa, A.
Thinn, Netalia, C.
Agostino, Michael, J.
Worthan, Neil
Worthan, Neil
Worthan, Mell
Worthan, Mell
Worthan, Milasbeth
Nomass OF SEQUENCES: 6
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 RVALTEDRIPRIBEIRIWGPLOEDADIOV 329
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APPLICATION NUMBER: US/09/978,979
FILING DATE: 16-00-2001
CLASSIFICATION: <Unknown>
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-978-979-6
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REGISTRATION NUMBER: 32,345
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CITY: Parsippany
STATE: New Jersey
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TYPE: amino acid
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Patent No. US20020151702A1
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ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SWGPRSPCSRSCGGGGVVTRRRQCNNPRPAFGGRACVGADLQARMCNTGACEKTGLEFMSQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 EYUTFLIVIPNLTSVYIANHRPLFTHLAVRIGGRYVVAGRASISPNTYPSLLEBGRVEY 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 SWGPRSPCSRSCGGGVVTRRRQCNNPRPARGGRACVGADLQAEMCNTQACEKTQLEPNSQ 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 OCARIDGOPLESSPGGASFYHWGAAVPHSQGDALCRHMCRAIGESFIMKRGDSFLDGTRC 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    532 MPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAR 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 MPSGPREDGTLSLCVSGSCRTFGCDGRNDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592 EYVTFLTVTPNLTSVYIANHRPLFTHLAVRIGGRYVVAGKMSISPNTTYPSLLEDGRVEY 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRCRSLVELTPIAAVHGRWS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                      352 LDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRCRSLVELTPIAAVHGRWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0, Gaps
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Pred. No. 2.8e-124;
1; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                 Score 1799; DB 9; Length 365;
Pred. No. 2.8e-124;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     652 RVALTEDRIPRIBEIRIWGPLORDADIQV 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 RVALTEDRIPRIERIRINGPLOEDADIOV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INTENTION, Agreemans Molecules
TITLE REPRESENTED 1501, 2015, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 1817, 18
               TYPE: amino acid
STRANDEDNESS: unknown
TYPOPLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC FEATURE
LOCATION: (365)..(365)
OTHER INFORMATION: unknown amino acid
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OTHER INFORMATION: unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/10057487
Publication No. US20030105313A1
GENERAL INFORMATION:
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Best Local Similarity 99.7%;
Matches 328; Conservative 1
                                                                                                                                                                                                                                                                                         Query Match 23.2%;
Best Local Similarity 99.7%;
Matches 328; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: homo sapiens
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35-10-057-487-5

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F007 TF:00:00 0T

US-09-978-979-5

-----RAGLAWSPC 288

Length 738;

US-10-057-487-5

à

FEATURE: PEATURE:

PPARAGECARCEDPSEKKKSECWPPT	PRIOR PLING DATE: 2000-10-18
MOLLISTICSACKA-	SOFTWARE: Patentin version 3.1
	SEC ID NO 8
10.1 SPALSORYTGALWOPPROGRAPHPANAKIGLYYSANBOCRVARGERANGEL 179	TIPE: FRI ORGANISM: homo sapien FRATURE:
DNCOALSCHIDPLDQSSCSRILVPILDGTECGVERNCSKGRCRSLVELTPIAAVHGRMSS	NAME/KRY: AISC FEATURE LOCATION: (43)
180	, NAME/KEY MISC FEATURE ; LOCATION: (1927(192)
193 GPSASPSSRPPKRAWICARPSPATOTRWIKAAAAASSPISMMGQN 237) OTHER INFORMATION: unknown amino acid
RAIGESFIMKRGDSFLDGTRC	LOCATION: (255)(255) LOCATION: (255)(255) COTHER INFORMATION: unknown amino acid
238 VAWRGGARROOTISLVAGGCRTFGCDGRDGROOFFDRCQVCGGDNSTCSPRKGSFTAGRAR 591	FARLURE: NAME/KEY: MISC_FEATURE
	, FRATURE: , NAME/KEY: MISC_FEATURE
592 BYVIFLY FRITS WITS WITS WELL FFILL WAS GERY WAS GRANNED SPATIY POLLED SRVEY 651 291	; DOCKTION: (374)(374) ; OTHER INFORMATION: unknown amino acid ; FEATURE:
H	NAME/KRY: MISC FEATURE 1 DAME/KRY: MISC FEATURE 1 OTHER INFORMATION: unknown amino acid
303 -VLISRPRCATIRPARRESMSSCRNSAPGFTASRCAPPLAAPFBTIGVL 350 710 VWAAVRGP-CSVSCGAGLRWYNYSCLDQARKELVETVQCQGSQQPPAWPBACVLEPCPPY 768	PEATURE JOANE/KEY, MISC PEATURE LOCATION: (452)(452)
351 LYHTAKGMLCADTGAGPLARASSXSVETASSMGPGVCQVAP 391	OTHER INFORMATION: unknown amino acid ; FRATURE: NAME/KEY: MISC FRATURE
769 WAVGDFGPCSASCG	, DOCATION: (458), OTHER INFORMATION: unknown amino acid
	NAME/KEY: MISC FEATURE ; COCKTION: (475)(475) ; OTHER INFORMATION: unknown amino acid
449 SREXQLPPTKEVGTLPTTGLSSHTWRXGSEGAMSWLGRXASPLTPPTPFGWRAVVSSTEW 508 824 PQPCPARMEVSEPSSCTSAGGAGIALENBTCVFGADGLEAP 864	, PEATURE , NAME/KEY, MISC FEATURE , LOCATION: (487)(487)
	, CTHER INFORMATION: unknown amino acid
865 VIBGROSYDEKLPABBOUGKSCPROMGLIANTSAGEKASSPROGIETGADANIVETDA. 924	Chery Match Best Local Similarity 39.4%; Pred, Nc Matches 374; Conservative 34; Misma
GSCSVSCGRCLMELRFLCMDSALRVPVQEELCGLASKPGSREVCQAVPCPARMQYKLAA	Oy 252 SPGLBHDGA-PGSCGPGHVMABGGAAF
GSCSVSCGRGLMELRFLCMDSALRVPVQEELCGLASKRGSRREVCQAVPCE	
985 CSWSCGRGWWRILYCARAHGEDDGEELLDTQCQCDPRPEPQBACSLEP 1034	Oy 289 SRRQLUSI
COVOCCROVYNRALIACORCORDINALIACORCORCORDINALIACORCORDINALIACORCORDINALIACORCORDINALIACORCORDINALIACORCORDINALIACORCORDINALIACORCORCORCORCORCORCORCORCORCORCORCORCORC	303
RRSULT 9 US-10-057-487-6	Db 121 SRALSQRWTGALVWDPPRPQPGSAGHB
Sequence 6, Application US/1005/487 Publication No. US/20030105313A1	Oy 353 DMCQALSCHTDPLDQSSCSRLLVPLLDC
Ayensing: Nyesing Nyesing	Db 180
11:11E REFERENCE: 08702-0071 PILE REFERENCE: 08702-0071 THERENT APPLICATION NUMBER: 15/10/057.487	Oy 413 WGPRSPCSRSCGGGVVTRRRQCNNPRPA
LING DATE: 2002-01-25	DD 193 GPSASPSSRPPKRAWICARPSPA

IOR APPLICATION NUMBER: 60/241,469
MOR PLLING DATE: 2000-10-18
MBER OF SEQ ID NOS: 8
FTWARE: Patentin version 3.1

252 SFGLEHDGAPGSGCGPSGHVMASDGAAP------RAGLAWSPC 288 1 SFGLEHDGAPGSGCGPSGHVMASERRRPAPASPGPPAAAGSCXACSDPSLRRSLCWPPT 60 302 61 SAPAGALVIVPAKSRILVGGAGREILFPLTKGHASKRFHPRAHSSVPPPFGVHPGTEPGL 120 303 ------RCVWDPPRPQPGSAGHPPDAQPGLYYSANEQCRVAFGPKAVACTFAREHL 352 121 SRALSORWICALVWDPPROPGSAGHPRNAHLGLYYSANBOCRVAFGPRAVACTFARBH- 179 353 DMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRCRSLVELTPIAAVHGRWSS 412 113 WGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTOLEFMSQQ 472 193 GPSASPSSRP-----PKRAWICARPSPA-----TOTRWIKAAAAASSPLS#MGGN 237 ary Match 18.8%; Score 1459.5; DB 14; Length 738; Local Similarity 39.4%; Pred. No.7.7.99-9.5; Local Similarity 34.4%; Pred. No.7.7.99-9.5; Chees 74; Conservative 34; Mismatches 163; Indels 379; Gaps 289 SR------RQLLSLLSAGRA-----

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59 SCLIGALEPGAVSSYLSPGAPLKGRPPSPGFORQRQRRAAGGILHLELLVAVGPDVFQA 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 HQEDTERYVLINLNIGAELIRDPSLGAQFRVHLVOVVILTEPBGAPNITANLTSSLLSVC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 SCLOALEPQAVSSYLSPGAPLKGRPPSPGFORORORRAAGGILHLELLVAVGPDVFQA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 HOEDTERYVLTNINIGAELLRDPSLGAQFRVHLVKKVILTEPEGAPNITANLISSLLSVC 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SCLÓALEPQAVSSYLSPGAPLKGRPPSPGPGRQRQRQRRAAGGILHLELLVAVGPDVPQA 62
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16.3%; Score 1561; DB 14; Length 342;

Bost Local Similarity 10.0%; Pred. No. 76-88.

Mitches 239; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.3%; Score 1261; DB 9; Length 242;
100.0%; Pred. No. 7.6e-85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. ...
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/241,469
FILING DATE: «Unknown»
                                                                                                                                                                                                                                                                         NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,345
REFERENCE/DOCKET NUMBER: GI 5435p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wyeth
IIILE OF INVENTION: Aggrecanase Molecules
FILE REFERENCE: 08702.0073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/057,487
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: 60/241,469
PRIOR FILING DATE: 2000-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 660-5000
TELEFAX: (973) 683-4117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10057487
Publication No. US20030105313A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 242 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELBEAK: (973) 683--
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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Best Local Similarity 100:0
Matches 239; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 242
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                                                                  173 CARTDGQP-LRSSFGGASFYHWGAAVPHSQGDALCRHNCRAIGESPIMKRGDSFLDGTRC 531
                                                                                                                                                                     532 MPSGPREDGTLSLCVSGSCRTFGCDGRMDSOOVWDRCOVCGGDNSTCSPRKGSFTAGRAR 591
                                                                                                                                                                                                                                                                                                                                                                                                  262 MGAG-----SPGGGSAT---- 29APAREVW------SPGGGSAT---- 290
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Totale, Monalise C.

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Patent No. US20020151702A1
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196 QKYYLTGGWSIDWPGEPP-~PACTTPEYQRSFN-----RPERLYAPGPINETLVPEILMQ 848
                                                                                 684 YGEBYGNLTRPDITFTYFQPX-----PRQAWVWAAVRGPCSVSCGAGLRWUNYSCL 734
                                                                                                                                                                            B49 -GK-----NPGIAWKYALPKVMNGTPPATRRPAYTWSIVQSECSVSCGGGYINVKAICL 901
                                                                                                                                                                                                                                                              135 DQARKELVETVQCQGSQQPPAMPEACVLEPCPPYWAVGDFGPCSASCGGLRERPVRCVE 794
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Deal Similarity 25.54; Score 1176.5; DB 9; Length 1629;
Bset Local Similarity 25.54; Pred. No. 1.7e-7.7
Matches 348; Conservative 170; Marantches 569; Indels 343; Gape
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Patent No. US20020090373A1
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NUMBER OF SEQ ID NOS: 10
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                                                      CWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDIG 238
                                                                                                                               123 GWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGGACSPTWSCLITEDTG 182
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                                                                                                                                                                                                                          239 FDLGVTIAHEIGHSFGLEHDGAPGSGCGPSGHVMASDGAAPRAGLAWSPCSRRQLLSLL 297
                                                                                                                                                                                                                                                                                                            183 POLGVIIAHEIGHSPGLEHDGAPGSGCGPSGHVMASDGAAPRAGLAWSPCSRROLLSLL 241
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Local Samilarity 28 44, Score 1190.5; DB 14; Length 1221;
Best Local Samilarity 28 44, Pred. No. 1.1.e-7, Marche 23, Conservative 139, Mismatches 409, Indels 237, Gape
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TITLE OF INVENTION: No. 1052030315828Alai aggrecanase
FILE REFERENCE: 08959-0008. US/10/240.545A
CURRENT FLIME DATE: 2002-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR PALLCATION NUMBER: PCT/JF01/11033
PRIOR PLIND DATE: 2001.22.17
PRIOR APPLICATION NUMBER: 0P 2000-384300
PRIOR APPLICATION NUMBER: 0P 2000-384300
NUMBER OF SEQ ID NOS: 26
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Publication No. US20030185828A1
GENERAL INFORMATION:
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TECGVERMCSKGRCRGLVELTPIAAVHGRWSSWGPRSPCSRSCGGGVVTRRRQCNNPRPA 440 PGGRACVGADLQAEMCNTQACEKTQLEFMSQQCARTDGQPLRSSPGGASFYHWGAAVPHS 500 TECEPGKHCKKGFC--VPKEMDVPVTDGSWGSWSPFGTCSRTCGGGIKTAIRECNRPEPK 568 NGGKYCVGRRMKFKSCNTEPCLKQKRDFRDGCAHFDGKHFNIN-GLLPNVRM---VPKY 624 TYPE: PRT ORGANISM: Homo sapiens ADAMTS-9 LOCATION: (468) OTHER INFORMATION: Xaa = Cye NAME/KEY: MOD_RES , OTHER INFORMATION: Xaa = Tyr US-09-918-171A-13 NUMBER OF SEQ ID NOS: 31 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 13 GENERAL INFORMATION: NAME/KEY: MOD RES LOCATION: (468) US-09-918-171A-13 LENGTH: 1882 LOCATION: FEATURE: ò a ò ò a ò 8 ò +89 ECSKSCDGGTQRRRAICVNTRNDV---LDDSKC---THQEKVTIQRCSEFPCF-QWKSGD 1041 042 WSECLVTCGKGHKHRQVWCQPGEDRLNDRMCD-----PETKPTSMQTCQQPECASW 1092 1093 -----QAG----PW------GQCSVICGQGYQLRAVKCIIGTYMSVV 1124 125 DDNDCNAATRPTDTQD-CELPSCHPPPAAPETRRSTYSAPRTQWRFGSWTPCSATCGKGT 1183 994 VRILYCARAHGEDDGEEILLDTQCQGLPRPEPQEACSLEPCPPRWKVMSLGPCSASCGL 1053 184 RMRYUSC-----RDENGSVADESACATLPRPVAKEECSVTPC-GQWKALDWSSCSVTCGQ 1237 054 GTARRSVACVQLDQGQDVEVDEAACAALVRPEASVPCLIADCTYR------- 1098 .238 GRATRQVMCVNY ---SDHVIDRSECDQDXIPKTDQDCSMSPCPQRTPDSGLAQHPFQNED 1294 ------WHVGTWMECSVSCGDGIQRREDTCLGPQAPVPADFCQHLP 1140 295 YRPRSASPSRTHVLGGNOWRTGPWGACSSTCAGGSQRRVVVC---ODENGYTANDCVERI 1351 931 OCGLGYRILDIYCAXXSRLD-GKIEKVDDGFC-SSHPKPSNREKCSGBCNIGGHRYSAWT 988 DAQPGIYYSANEQCRVAPGPKAVACTPAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDG 380 TECGVERWCSKGRCRSLVELTPIAAVHGRWSSWGPRSPCSRSCGGGVVTRRRQCNNPRPA 440 103 NGGKYCVGRRMKFXSCNTEPCLXOKRDFRDEOCHPDGKHFNIN-GLLPNVRM----VPKY 658 QGDAL---CRHNCRAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDG 557 559 SGILMKDRCKLFCRVAGNTAXYOLRDRVIDGTPC-----GODTNDICVOGLCROAGCDH 712 558 RMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRARBYVTFLTVTPNLTSVYIANHRPLPT- 616 113 VLNSKARRDKCGVCGGDNSSCKTVAGTFNTVH-YGYNTVVRIPAGATNIDVRQHS--FSG 769 17 -----HLAUR------IGGRYUVA-GKOMSISPNITYPSLLEDGRVEYRVALTEDRLPR 662 770 ETDDDNYLALSSSKGEFLLNGNPVVTMAKREIR-----IGNAVVEYSGSET----A 816 563 LEEIRIMGPLOSDADIQVYRRYGEEYGNLTRPDITFTY---FQPKPRQAWVW----- 711 317 VERINSTDRIEGELLLQVL----SVGKLYNPDVRYSFNIPIEDKPQQ-FYWNSHGPWQA 870 AAVRGPCSV 720 971 CSKPCQGERKRKLVCTRESDQLTVSDQRCDRLPQPGHITEPCGTDCDLRWHVASRSECSA 930 721 SCGAGLRWVN-----YSCLDQARKELVETVQCQGSQQPPAWPEACVLEPCPPYWAVGDFG 775 PCSAS CGGGLRERPVRCVEAQGSLLKTLPPARCRAGAQQPAVALETCNPQPCPARWEVSE 835 836 PSSCTSAGGAGLALENETCVPGADGLEAPVTSGPGSVDEKLPAPEPCVGMSCP----PGW 891 GHLDATSAGEKAPSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGLMELRFLCMDSALRVPV 951 952 OEELCGLASKPGSRREVCQAVPC---PA------RWQY-KLAACSVSCGRGV 993 207 ELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPGSGCG 266 75 CRAHDKCDTLGLABLGTICDPYRSCSISBDSGLSTAFTIAHBLGHVFNNPHD--DNNKCK 432 267 PSG----HVMASDGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQPGSAGHP-P 320 433 EBGVKSPQHVMAPTLNPYTNPMMSKCSRXYITEFLDTGYGECLLNEPESRP----YPLP 488 489 VOLPGILYNVÄKÖCELIEGPGSOVČPYMO----ÖRRIMCNNVNGVHKGCRIOHTPWADG 544 45 TECEPGKHCKYGPC--VPKEMDVPVTDGSWGSWSPFGTCSRTCGGGIKTAIRECNRPEPK 602 441 FGGRACVGADIQAEMCNTQACEKTQLEFMSQQCARTDGQPLRSSPGGASFYHWGAAVPHS 500 141 KPVTVRGCWAGPCV--377

APPLICANT: When the state of th Sequence 13, Application US/09918171A Patent No. US20020110894A1

89 ORORORRAAGGILHLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLADPSLGAQFR 148 IVIVALIVIHABQDGBSISFNAQTTLKAFCQW-----QHSNSPGGIHHDTAVLLTRQDI 340 455 VQLPGILYNVNXQXELIPGPGSQVCPYMMQ----CRRLWCNNVNGVHKGCRTQHTPWADG 510 207 ELPDGNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPGSGCG 266 341 CRAHDKCDTLGLABLGTICDPYRSCSISEDSGLSTAFTIAHBLGHVPNMPHD--DNNKCK 398 267 PSG-----HVMASDGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQPGSAGHP-P 320 399 EEGVKSPOHVMAPTLNPYTNPWMSKCSRKYITEFLDTGYGECLLNEPESRP----YPLP 454 DAQPGLYYSANEQCRVARGPKAVACTPAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDG 380 227 KRIHRRIKRFLSYPRPVEVLVVADNRAVSYHGENLOHYILTLMSIVASIYKDPSIGNLIN 286 149 VHLVKKVILTEPEGAPNITANLISSLLSVCGWSQTINPEDDTDPG--HADLVLYITRFDL Query Match
14.9%; Score 1157; DB 9; Length 1882;
Matches 3set Local Statiarity 5:4; Pred. No. 5.76-76;
Matches 3set, Conservative 179; Mismatches 505; Indels 342; Gaps

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956 CSKSCDGSTQRRRAICVNTRNDV---LDDSKC---THQBKVTIQRCSEPPCP-QWKSGDW 1008 1009 SECIVITCGKGHXHSQVWCQFGEDRINDRMCD-----PETKPTSMQTCQQPECASW- 1058 .059 -----QAG-----PW-------VQCSVTCGQGAQLRAVKCIIGTYMSVVD 1091 .092 DNDCNAATRPIDIQD-CELPSCHPPPAAPBTRRSTYSAPRIÇMRPGSWIPCSATGGKGTR 1150 995 RRILYCARAHGEDDGEBILLDTQCQGLPRPEPQEACSLEPCPPRWKVMSLGPCSASCGLG 1054 .055 TARRSVACVQLDQGQDVBVDBAACAALVRPBASVPCLIADCTYR------ 1098 1205 RATROVACYNY---SDHYIDRSECHODYIPETHONCOMSPCPORTPHSGLAQHPFQNEDY 1261 1099 ------WHVGTWMECSVSCGDGIQRRRDTCLGPQAQAPVPADFCQHLPK 1141 1262 RPRSASPSRIHVIGGNOWRIGPWGACSSTCAGGSGGRVVVC---GDENGYTANDCVERIK 1318 1142 PVTVRGCWAGPCV----- 1161 1319 PDEGRACESGPCPGWAYGNWGECTKLCGGGIRTRLVVSQRSNGERFPDLSCEILDKPPDR 1378 1162 -----VPHBEAAAPGRTTATPAGACGR-----QHLE-----PTGT 1191 1379 EQCNTHACPHDAAMSTGPWSSCSV-SCGRGHKQRNVYCMAKDGSHLESDYCKHLAKPHGH 1437 893 HIDATSAGEKAPSPWGSIETGAQAAHVWTPAAGSCSVSCGRGIMELRFICMDSALRVPVQ 952 837 SSCISAGGAGLALENETCVPGADGLEAPVTEGPGSVDEKLPAPEPCVGMSCP----PGWG 892 953 BELCGLASKPGSRREVCGAVPC---PA-----RWQY-KLAACSVSCGRGVV 994 625 SGILMKDRCKLFCRVAGNTAYYQLRDRVIDGTPC-----GQDTNDICVQGLCRQAGCDH 678 3.9 VLNSKARRDKCGVCGGDNSSCKTVAGTENTVH-YGYNTVVRIPAGATNIDVRQHS--FSG 735 617 -----HLAVR------IGGRYVVA-GKMSISPNTTYPSLLEDGRVEYRVALTEDRLPR 662 31 STDDDNYLALSSSKGEFLINGNFVVTWAKREIR-----IGNAVVEYSGSET----- 782 838 SKPCGGERKRKLVCTRESDQLTVSDQRCDRLPQPGHITEPCGTGCDLRWHVASRSECSAQ 897 729 -----VNYSCLDQARKELVETVQCQGSQQPPAMPEACVLEPCPPYMAVGDFGP 776 998 CGLGYRTLDIYCAKYSRLD-GKTEKVDDGFC-SSHPKPSNREKCSGECNTGCWRYSAWTE 955 777 CSASCGGGLRERPURCVEAQGSLLKTLPPARCRAGAQQPAVALETCNPQPCPARWEVSEP 836 558 RMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAREYVTFLTVTPNLTSVYLANHRPLFT- 616 663 LEEIRIWGPLQEDADIQVYRRYGEEYGNLTRPDITFTY---FQPKPRQAW-----VWAAV 714 1192 IDMRG------PGQADCAVAIGRPLGEVVTLRVLESSLNCSAG 1228 1438 RKCRGGRCPKWKAGAWSQCSVSMGR-----GVQQRHVGCQIG 1474 715 RGPC----SVS----Search completed: March 13, 2004, 08:07:02 Job time : 119:1 secs 용 음 요

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149 VHLVRAVILITEPEGAPNITANEISSLLSVCGWSQTINPEDDIDPG--HADLVLYITRFDL 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 WIVDWPGRYKFS-GTIF-----DYRRSYNEP-----SNLIAIGPINETLIVELLFQ 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGILHLELLVAVGPDVPQAH-QEDTERYVLTNINIGAELLRDPSLGAQFRVHLVKMVILT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GRPTRPKAPSHSAPLLGLALLRMHQRHPRARCPPLCVAGILACGPLLGCWGPSHFQQSCL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALEPQAVSSYLSPGAPLK---GR-----PPSPG------FORORORGRAA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 OPLH----SSDLRLGLPOKOHFCGRRKKYMPOPPKEDLFILPDBYKSCLRHKRSLLRSHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576 KYGDEGP-KPTHGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKRCEGSTRTLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 14.8%; Score 1148.5; DB 4; Length 1224; Best Local Similarity 28.3%; Peredi No. 239.84; Asserbed 28.1; Mismatches 43; Indels 241; Matches 143; Landels 241; Astrone 28.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1224
TYPE: PRT
ORGANISM: homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRILYCARAHGEDDGESILLDTQCQQLPRPEPQEACSLEPCPPRWKVMSLGPCSASCGLG 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRYVSC-----RDENGSVADESACATIPRPVAKEBCSVTPC-GQWKALDWSSCSVTCGQG 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .055 TARRSVACVQLDQGQDVEVDEAACAALVRPEASVPCLIADCTYR------- 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----WHVGTWMECSVSCGDGIQRRRDTCLGPQAQAPVPADPCQHLPK 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1142 PVTVRGCWAGPCV----- 1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           009 SECLVICSKGHKHSQVWCQFGEDRLNDRMCD------PETKPTSMCTCQQPECASW- 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .059 -----QAG-----PW---------VQCSVTCGQGYQERAVKCIIGTYMSVVD 1091
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                                                                                      TECRPSKHCKKGPC - VPKEMDVPVTDGSWGSWSPGTCSRTCGGGIKTAIRECKRPEPK 568
                                                                                                                                                                             PGGRACVGADLQAEMCNIQACEKTQLEFNSQQCARIDGQPLRSSPGGASFYHWGAAVPHS 500
                                                                                                                                                                                                                                                                   NGGKYCVGRRMKFKSCNTEPCLKQKRDFRDEQCAHFDGKHPNIN-GLLPNVRW---VPKY 624
                                                                                                                                                                                                                                                                                                                                                                    OGDAL --- CRHMCRAIGESFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDG 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                          525 SGILMKDRCKLPCRVAGNIAYYQLRDRVIDGIPC-----GQDINDICVQGLCRQAGCDH 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAREYVTFLTVTPNLTSVYIANHRPLFT- 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::|: |:| ||||||||:|
579 VLNSKARRDKGGVCGGDNSSCKTVAGTFNTVH-YGYNTVVRIPAGATNIDVRQHS--PSG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----HLAVR-----IGGRYVVA-GKMSISPNTTYPSLLEDGRVEYRVALTEDRLPR 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEEIRIMGPLOEDADIQVYRRYGEEYGNLTRPDITFTY---FQPKPRQAW-----VWAAV 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERINSTDRIEGELLLQVL----SVGKLYNEDVRYSFNIPIEDKPQGFYWNSHGPWQAC 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      955
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TECGVEKWCSKGRCRSLVELTPIAAVHGRWSSWGPRSPCSRSCGGGVVTRRRQCNNPRPA 440
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124 CNEHAC-TWWOFGVWSDCSAKCGDGVRDANC---TDRHRSVLPEHRCLKMEKI-ITKP 1178 942 CMDSALRVPVQEELCGIASKPGSRREVCGAVPCPARMQYKLAACSVSCGRGVVRRILYCA 1001 CV-SGNGTEVDMSLCGTASDRPASHOTCNLGTCPFWRNTDWSACSVSCGIGHRERTTECI 1268 002 RAHGEDDGEBILLDTQCQGLPRPEPQEACSLEPCPPRWKVMSLGPCSASCGLGTARRSVA 1061 269 YREQSVDA-----SFCGDTXOMPETSQTCHLLPC-TSWKPSHWSPCSVTCGSGIQTRSVS 1321 CVQLDQGQDVEVDEAACAALVRPEASVPC-----LIADC-TYRWHVGTWMEC 1107 CTRGSEG--TIVDEYFCDRNTRPRLKKKTCEKDTCDGPRVLQKLQADVPPIRWATGPWTAC 1379 956 IDCSTRWITEDV-SSCSAKCGSGOKRORVSCVKWEGDRGTPASEHLCDRNSKPSDIASCY 1014 015 IDCSGRKWNYGEWISCSETCGSNGXWHRKSYCVDDSNRRVDESL-C-GREGKEAIERECN 1072 1073 RIPC-PRWVYGHWSECSRSCDGGVWARHAQCLDAADRETHT---SRC-----GPAQTQEH 1123 179 CHRESCP-----KYKLGE-------WS----QCSVSCEDGWSSRRVS 1209 882 CVGMSCPPGWGHLDATSAGEKAPSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGLMELRFL 941 362 TDPLDQSSCSRLLVPLLDGTECGVEK--WCSKGRCRSLVELTP--IAAVHGRWSSWGPRS 417 557 TFYGSCMGCRIQHMPWADGIPCDESRSMFCHHGAC---VRLAPESLIKIDGCWGDWRSWG 613 418 PCSRSCGGGVVTRRRQCNNPRPAFGGRACYGADLQAEMCNTQACEKTQLEFMSQQCARTD 477 478 GQPLRSSPGGASFYHWGAAVPHSQGDALCRHMCRAIGESFIMKRGDSFLDGTRCMPSGPR 537 574 NKDIGIQGVASTNIHWVPKYANVAPNERCKLYCRLSGSAAFYLLRDKVVDGTPCDRNGD- 732 538 EDGTLSLCVSGSCRIFGCDGRMDSQQVWDRCQVCGGDN8TCSPRKGSFTAGRAREYVTFL 597 733 -----DICVAGACMPAGCDHQIHSTLRRDKCGVCGGDDSSCKVVKGTFNEGGTFGYNEVM 787 598 TVTPNLTSVYIA-----NHRPLFTHLAVR-IGGRYVVAGKAKISPNTTYPSLLEDGRVBY 651 88 KIPAGSANIDIROKGYNNMKEDDNYLSLRAANGEFILMGHPQVS-LARQOIAFQDTVLEY 846 552 RVALTEDRIBERIRIMGPLOEDADIQVYRRYGERYGNLTRPDITFTY-----FQ 702 03 P-----KPRQA---- 708 896 PISSALYLMRVIDIWIECDRACRGQGSQKLMCLDMSTHRQSHDRNCQNVLKPKQATRMCN 955 728 CLDGARKELVETVÇÇĞĞĞQPPAMPBACV 761 762 LEPCPPYWAVGDFGPCSASCGGGLRERPVRCVEAQGSLLKTLPPARCRAGAQQPAVALET 821 822 CNPOPCFARMEVSEPSSCTSAGGAGLALENETCVPGADGLEAPVTEGPGSVDEKLPAPEP 881 WDPPRPQPGSAGHPPDA----QPGLYYSANBQCRVAPGPRAVACTFAREHLDMCQALSCH 361 505 PD----QPVERRYYEDVPVRDEPGKKYDAHQQCKFVPGPASELCPY----MPTCRRLWCA 114 ECSRICGGGVQKGLRDCDSPKPRNGGKYCVGQRERYRSCNIQECPWDIQPYREVQCSEFN 109 -----WUNRAURGPCSVSCGAGLR-----1108 SVSCGDGIQRRRDTCLGPQAQAPVPADFCQHLPKPVTVRGCWAGPC 1153 1380 SATCGNGTGRELLKC--RDHVRDLPDEYCNHLDKSVSTRNCRLRDC 1423 g g 6 ò à 9 ò g à g ò 8 ક 合 ò ò -----AECSHICGKGWRKRAVACKSINPSARAQLLPDAVCISEPKP-RMHEACLLQ 1045 PC--PARMOYKLAA---CSVSCGRGVVRRILYCARAHGEDDGEEILLDTQCQGLPRP--E 1025 1046 RCHKPKKLONLVSAMSQCSVTČERGTOKRFLKČAEKYVSGKYRE-LASKKČSHLPKPSLE 1104 1026 POERCSIEPCPPRWKVMSLGP------CSASCGLGTARRSVACVQLDQGQDVEV 1073 1105 LERACAPLPCPRHPPFAAAGPSRGSWFASPWSOCTASCGGGVCTRSVQC--LAGGRPA-- 1160 327 VVVKLIVLKTENAGPRITQNAQQTLQDFCRWQQYYNDPDDSSVQHHDVALLLTRKDICRS 386 210 DGNRQVRGVTQLGGACSPTWSCLITEDTGPDLGVTIAHEIGHSPGLEHDGAPGSGCGP-- 267 987 GEKEDILGIAELGIMEDMQKSCALIEDNGLSAAPIIAHELGHVPSIPHDDE--RKCSTYM 444 -----SGHVMASDGAAPRAGLAWSPCSRRQLLSLL--SAGRARCV 305 916 AAHVWTPAAGSCSVSCGRGLMBLRPLCMD----SALRVPVQEBLCGLASKPGSRREVCQAV 972 91 GRGRGRRAAGGILH-LELLVAVGPDVFQAHQEDTERYVLTNINIGAELLRDPSLGAGFRV 149 150 HEVKAVILTEPEGAPNITANLTSSELSVCGWSQTINPEDDTDPGHADLVLYITRFDLELP 209 384 YGEEYGNLTRPDITFTYF-----QPKPRQAWVWAAVRGFCSVSCGAGLRWVNYSCLD 735 G-----RNPGVAWEYSMPRIGIEKÖPPAQPSYTWAIVRSECSVSCGGGGMTVREGCYR 898 736 QARKELVETVQCQGSQQPPAMPEACVLEPCPPYWAVGDPGPCSASCGGGLRERPVRCVEA 795 399 DLKFQ-VNMSFCNPKTRPVTGLVPCKVSACPPSWSVGNWSACSRTCGGGAQSRPVQCTRR 957 796 QGSLIKTLPPARÇRAGAQQPAVALETCNPQPCPARWEVSEPSSCTSAGGAGLALENETCV 855 958 VHYDSEPVPASLC------9QPAPS------976 356 PGADGLEAPVTEGPGSVDEXLPAPEPCVGMSCPPGWGHLDATSAGEKAPSPWGSIRTGAQ 915 267 RKARSRRAANSWDHYVEVILVVADTKOYEYHGRSIEDYVLTLFFFTVASIYRHQSLRASINV Gaps Owery Match 14.4%; Score 1118, DB 4; Length 2165; Seet Local Similarity 26.6%; Pred. No. 1.6e-81; Matches 331; Conservative 147; Mismatches 501; Indels 272; CHESTAL INFORMATION 13 Name secreted proteins of the protein of th Sequence 155, Application US/09800729 Patent No. 6605592 1074 DEAACAALVRPEASVPC 1090 1161 --SGCLLHQKPSASLAC 1175 TYPE: PRT ORGANISM: Homo sapiens 18-09-800-729-155 SEQ ID NO 155 S à a à 8 음 ò a ò g ò

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gene encoding the same, pharmaceutical of immunologically analyzing human ADAWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 PPSPGRORORORGRAAGGILHLELLVAVGPDVPQAHQEDTERYVLTWLNIGAELLRDPS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       948 CKSA----DORSTLPPGHCLPAARPSTWRCNLRRCPPARWVTSEWGECSTOCGLGQQQR 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1004 TVRCTS-HTGQ----PSRECTEALRP------SINGGCEAKCDSVVPPG 1041
                                                                                                                                                                                                                                                                                                                                  855
                                                                                                                                                                                                                                                                                                                                                                                                                 760 CVLEPCPPYWAYGDPGPCSASCGGGLRERPYRCVEAGGSLLKTLPPARCRAGAGGPAVAL 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              820 ETCNPQPCPARWEVSEPSSCTSAGGAGLALENETCVPGADGLEAPVTEGPGSVDEKLPAP 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     903 SAC-POPRP------PVL 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    880 EPCVGMSCPPGWGHLDATSAGEKAPSPWGSIRTGAQAAHVWTPAAGSCSVSCGRGLMELR 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           914 BACHGPICPPEWATLD------ 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   940 FLCMDSALRVPVQEELCGLASKPGSRREVCQAVPCPARWQYKLAACSVSCGRGVVRRILY 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 930 -----SECTPSCGPGLRHRVIL 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1000 ÇARAHGEDDGEETLIDTQCQGLPRPEPQEACSLEPCPP-RWKVMSLQPCSASCGLGTARR 1058
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                                                                                                                                                                                                                                                                                                                 797 ARDSLPPYSWHYAPWT-KCSAQCAGGSCVQAVECRNQLDSSAVAPHYCSAHSKLPKRQRA
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12.1%; Pred. No. 1.6e-67;

Conservative 102; Mismaches 334; Indels 117; Gaps
                                                                                                                                                                                                                                                    104 ----KPROAWWAAVRGPCSVSCGAGLRWVNYSCLDQARKELVETVQCQGSQQPPAMPEA
90 SPASPGAGYEDVVWIPKGSVHIFIQDINLSLSHLALKGDQESILLBGL---PGTPQPHRL
                                                                                       345 EDGRVEYRVALTEDRIPRIBEIRINGPLQEDADIQVYRRYGEEYGNLTRPDITFTYFQP-
                                                                                                                                                                     747 PLAGTTFQLRQGPDQVQSLBAL---GPINASLIVMVLAR-----TELPALRYRFNAPI
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TITLE OF INVENTION: Human ADAMTS-1 protein,
TITLE OF INVENTION: composition and method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFRENCE: 05/092 """
CURRANT PALLANION UNGBER: US/09/445,023A
CURRANT FILMS DATE: 1999-12-03
PRIOR PARLICATION WINGER: 19 9-160422
PRIOR PARTE: 1997-66-03
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Patent No. 6565858
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SOFTWARE: Patentin version 3.0
SEQ ID NO 12
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US-09-445-023A-12
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Best Local S:
Matches 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 IA-----HEIGHSPGLEHDGAPGSGCGPSGH----VMASDGAAPRAGLAWSPCSRRQLL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 AATSVHHCHEIGHTPGMAHDGV-GNSCGARGQDPAKLMAAHITMKTNPPVMSSCNRDYIT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 SILSAGRARCVWDPPRPQPGSAGHPPDAQPGLYYSANEQCRVAFGPKAVACTFAREHLDM 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COALSCHIDPLDQSS-CSRLLVPLLDGTEC---GVEK-WCSKGRCRSLVELTPIAA---- 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 VHGRWSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQ 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   523 VDGAWGPWTPWGDCSRTCGGGVSSSSRHCDSPRPTIGGKYCLGERREHRSCKTDDCPPGS 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 LEFMSQQCARTDGQPLRSSPGGASFYHWGAAVPHSQGDALCRHMCRAIGESFIMKRGDSF 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ODPREVOCABROSIPPR----GKPYKW--KTYRGGGVKACSLISLAEGFNPYTERAAAV 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526 IDGTROMPSGPREDGTLSLCVSGSCRTFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSF 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 VDGTPCRPD----TVDICVSGECKHVGCDRVLGSDLREDKCRVCGGDGSACETIEGVF 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 RVSVEYWTREGLAWQRAARPHCLYAGHLOOQASSSHVAISTCGGLHGLIVADEBEYLIEP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PSPGRQRQRQRRAAGGILHLELLVAVGPDVFQAH-QBDTBRYVLTNINIGAE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 LLRDPSLGAQFRVHLVXWVILTEPEGAPNITANLISSILLSVÇGWSQTI-----NPEDD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 LFQDSSLGSTVNILVTRLILLTEDQPTLEITHHAGKSLDSFCKWQKSIVNHSGMGNAIPE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .90 TDPGHADLVLYITRPDL----ELPDGNRQVRGVTQLGGACSPTKS-CLITEDTGFDLGVT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420 SPLDSGLGLCLNNRP---PRODPVYPTVAPGQAYDADEQCRPCHGVKSRQCKYG----EV 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSELWC----LSKSNRCITNSIPAAEGTLCQTHTIDKGWCYKRVC-----VPFGSRPEG 522
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THE REFERENCE; ACTIVICATION OF THE CONTROL OF THE PROPERTY APPLICATION OF THE PRO
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                                                             Sequence 17, Application US/09369364A
Patent No. 6391610
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
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APPLICATION DATA.
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RATEMENT/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1211 amino acide
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8389-0900-888

LENGTH: 1211 amino acide TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear

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613 PLFTHLAVR--IGGRYVV-----AGKNGISPNTTYPSLLEDGRVBYRVALTEDRLPR 662
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                                                                                                                                                         91 ORGRORRANGGILHLELLVAVGPDVFQAH-OEDTERYVLTNINIGAELLRDPSLGAOFRV 149
                                                                                                                                                                                                                       554 RRRARRHAADDDYNEIVLLGVDDSVVQFHGKEHVQXYLLTLMNIVNEIYHDESLGAHINV 313
                                                                                                                                                                                                                                                                                                    150 HLVRAVILTEPEGAPNI-TANLTSSLLSVÇGWSQTINPEDDTDPGHADLVLYITRFDLEL 208
                                                                                                                                                                                                                                                                                                                                                          109 PDGNRQVRGVTQLGGACSPTWSCLITEDIGFDLGVTLAHEIGHSFGLEHDGAPGSGCGPS 268
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Query Match
11.94; Score 920; DB 4; Length 1211;
Best Local Similarity 27.84; Pred. No. 8.6e-6. Matches 28; Conservative 118; Mismatches 370; Indels 248; Gaps
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ZIP: 10036-2811 COMPUTER READABLE FORM: CSA COUNTRY:

Sequence 5, Application US/09491522 Patent No. 6428998 GENERAL INFORMATION:

663 LEBIRIWGPLQBDADIQVYRRYGBBYGNLTRPDITFTYF-------QPKFRQAW 709

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		Db 248 RRENREEADDDYNIEVILLOWDUSVVQFHOTENVKRILLIAMINELIINDELIIINDELIINDELIINDELIINDELIINDELIINDELIINDELIINDELIINDELIINDELIINDELIIINDELIINDELIINDELIINDELIINDELIIINDELIINDELIIINDELIIINDELIINDELIIINDELIINDELIII		208 LPDGNRQVRGVTQLGGACSPTWSCLITEDTGPDLGVTAAEIGHSPGLEHDGAPGSGCGP	366	OY 266 SGRIVAADGAAPRAGLAMEECERROLLELAGARAKUVNIPERROLESANAIFEDAM- 343 DD 422 EVRLASSIMAPLVOAAPREPINSRCSQQSLSRYLHSYDCLRDDPFTHDWFALPQL 475	Qy 324 PGLYYSANEQCRVARGERAVACTEARBHLDMCQALSCHTDFLDGSSCSRLLVPLLGGTBC 383	476 PGLHYSNNEQCRPDFGLGYYXCTAFKT-PDPCKQLMC-SHPDNPYFCKTKKGFPLDGTMC	Cy 384 GYBKKCSKGECKSLVELTFIAAVHGRNSSRGERFCSRSCGGGGVVFRACKTWARKAG 443 Db 534 AFGRECFKGRCTMLTFDILKRDGNWGANGFRGSCSRTCGTGVKFRTRQCDNFHPANGG 591	Gy 444 RACUGADIQAEMCNIQACEKTQLEEMSQCCARIDGGPLRSSPGGASFYHWGAAVPHSGGD 503	Db 592 RTCSGLAYDPQLCNSQDCPDALADFREEQCRQWDLYFEHGDAQ-HHWLPHEHRD 644	Qy 504 ALCRIMCRAIGBSFIMKRGDSFLDGTRCMPSGPREDGTLSLCVSGSCRTFGCDGRM 559	Do 645 AKERCHLYCESKETGEVYSMKRMYHDGTRCSYKDAFSLCVRGDCRKYGCDGVI 697	Oy 560 DSQQVWDRCQVGGDNSTCSPRKGSFTAG-PAARBYVFLTVFPNL7SVYJANHRPLFTHL 618 b 698 GSSKQBXCQVCQDNSSECKVVWQTPSRSPSRGAGTYRPFLTVRFPLIAGRADTTSHHL 757	Qy 619 AVRIGGRYVVAGKKSISPNT-TYPSLLEDGRYBYRVALTEDRLFRLEBIRI 668	Db 758 AVKNLETGKFILNEENDUDPNSKTFIAMGVEWBYRDEDGRETLQT 802	YPQPKPRQAWVW :	Db 803 MGPLHGTTTVLVIPEGDARISLTYKYMIHEDSLAVDDNNVLEDDSVGYEW 852	Qy 712 AAVR-GECSVSCGAGLRWYNYSCLDQARKELVETVQCGGGQPPAMPEACYLEPG-PFYM 769	770	DD 913 VTGEWEFCSRSCGRTGWQVRSVRCVQPLANNTTRSVHTYGHCNDARPEGRRACURELC 969	Cy 828 PARMEVSEPSCTSAGGAG 846	D5 970 PGRWRAGSWSQCSVTCGNG 988	RESULT 0 US-09-445-023A-1) Sequence 1, Application US/09445023A ; Parent No. 655588 ; GBNSRAL WRORMATION	APPLICANT: Hirose, Kunitaka APPLICANT: Inogushi Eiji APPLICANT: Hogothi Michinori	A APPLICANT: Indicate, Red ko A APPLICANT: Indicate, Vicako A APPLICANT: Meternealina, Kouji A APPLICANT: Muno Xouji A APPLICANT: Muno Xouji	
804 -ETLOTAGELMGTITVLIVIPVOD-TRVSLTYKYNIHEDSLAVTDONVLEEDGVYY 556 710 VARANG-GPÇGVSÇDAGLBWYNYSCILODARKELYSTVQCQGSQQPRARPACVLEPC-PP 767	BMALKKWSPCSKPCGGGSQFTKYGCRRKLDHOWHRGFCAALSKPKAIRRACNPDECSQP	768 YMAVQDFGPCSASCG-GGLRERFVPCVE-AQGSLLKTLPPARRRAGAQQPAVALETCNFQ 825 917 VAVTGBREPGSGCTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	826 PCFARWEVSEPSSCTSAGGAGLALENETCVPGADGLEARVTEGPGSVDEKLPAREFCVGM 885	974 LCPGRWRA	886 SCPPGWGHLDATSAGEKAPSPWGSIRTGAQAAHWYTBAAGSCSVSCGRGIMELRFICM 943	982GPW	1006 DDSFGI-CQEERPETAR-TCRLGPCPRNI 1032	1004 HGEDDGEEILLDTQCQGLPRPEPGRACSLEPCPRRKKWSLQPCSASCGLGTARRSVAC 1062	1033SDPSKKSYVVQWLSRPDPDSPIRKISSKGHCQGDKSIFC 1071	09-491-522-11	sequence 11, Application US/09491522 Patent No. 6428998	GENERAL INFORMATION: APPLICANT: Colide, Alain	APPLICANT: Daplere, Unalles M. APPLICANT: Prockop, Darwin J.	TITLE OF INVENTION: RECOGNISHING N-FROTEINAS. TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF UNDERSOLVENISHING. CORRESPONDING S. 17	ADPRESSE: Pennie & Edmonds, LLP STREET: 1155 Avenue of the Americae	CITY: New York STATE: NY	COUNTRY: USA ZIF 10056-2811 COMPITER PRINAIN PORM:	CONFICIENT TYPE: DISCRETE COMPINED: TEM Comments	CONTINENT SET CONTINUED OF SECRET SECURITY OF SECRET SECRET SECURITY SECURITY SECURITY SECURITY OF SECURITY SEC	COMMAN NUMBER: US/09/491,522 FILING DATE:	CLASSIFICATION: PRIOR APPLICATION DATA:	APPLICATION NUMBER: 04/046,533	NAME: Abrama, Samuel B REGISTRATION NUMBER: 30,605	REFERENCE/DOCKET NUMBER: 8389-0060-999 TELECOMMINICATION INFORMATION: TELEPHONE: 650-493-4935		BEQUENCE CHARACTERISTICS: LENGTH: 1.205 anino acids TYPE: anino acid	GTRANDENESS: single TOPOLOGY: linear -09-491-522-11	

4.194

77/ 000-00-8

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APPLICATIVE TRILERAN, DOUGHS A, APPLICATIVE TRANSCO-14, TANGO-15, AND TANGO-15, TANGO-15, TANGO-16, AND TANGO-15, TANGO-17, TANGO-17, TANGO-17, TANGO-17, TANGO-17, TANGO-17, TANGO-17, TANGO-17, TANGO-17, TANGO-18, TANGO-19, TA
                                                                                  Sequence 2, Application US/09130491
Patent No. 6416974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Homo sapiens
US-09-130-491-2
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 967
US-09-130-491-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Indels 134; Query Match 11.8%; Score 914; DB 4; Length 967; Best Local Similarity 29.7%; Pred Mo. 2e-65; Marches 238; Conservative 111; Mismatches 319; Indels 1 Marches 288; Conservative 111; Mismatches 319; Indels 1

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DGNR--QVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPG----S 263

122 CGSQTCDTLGMADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNAPHDDAKQCASLN 150 HLVKAVILIEPEGAPNITANLISSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLELP

65 VVVKILVIHDEOKGPEVTSNAALTIRNFCNWOKONNPPSBRBAEHYDTAILFTRODL--- 121

90 RORORORRAMGGILHLELLVAVGPDVFQAHQEDTERYVLTNLMIGAELLRDPSLGAGFRV 149

Owery Match 11.8%; Score 914.5; DB 4; Length 727; Best Local Similarity 29.9%; Pred. No. 1.2e-6, 1.00.4 States 246; Conservative 111, Mismatches 346; Indels 127, Gaps

SOFTWARE: Patentin version 3.0

ORGANISM: Homo sapiens 09-445-023A-1 SEQ ID NO 1 LENGTH: 727 TYPE: PRT

RIRLRKKRFVSSPRYUETWLVADOSMAEFHGSGLKHYLLTLFSVAARLYKHPSIRNSVSL

64

291 RLYKHPSIRNSVSLVVVKILLVIHDEQKGPEVTSNAALTLRNFCNWQKQHNPPSDRDAEHY 350 DLVLYITRFDLELEDGNR--QVRQVTQLGGACSPTWSCLITEDTGFDLGVTIAHBIGHSF DTAILFTRODL --- CGSQTCDTLGWADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVF 961

g

P---PDAQPGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLV 375

GCGFSGHVMAS-----DGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQPGSAGH 318

.82 GVNODSHMANSMLSNLDHSOP-----WSPCSAYMITSFLDNGHGECLMDKPQ-----N 230 PIQLPGDLPGTLYDANRQCQFTFGEDSRHCPDA---ASTCSTLWCTGTSGGVLVCQTMHP ROCHNPRPAFGGRACVGADLGAEMCNTQAC-EKTQLEFNSQQCARTDGQPLRSSPGGASF 490

344 RECDMPVPKNGGKYCEGKRVRYRSCNLEDCPDWNGKTPREEGC-EARNEPSKASFGSGPA

PLLDGTECGVEKWCSKGRCRSLVEL----TPLAAVHGRWSSWGPRSPCSRSCGGGVVTRR 431 287 PWADGISCGEGKWCINGKCVNKIDRKHPDIPF---HGSWGPWGPWGDCSRICGGGVQYIM 343

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:08 IANH-----RPLFTHLAVRIG-GRYVVAGKOMSISPNTTYPSLLEDGRVEYRVALTEDRLP 661

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254 GLEHDGAPG----SGCGPSGHVMAS-----DGAAPRAGLAWSPCSRRQLLSLLSAGRARC 304 408 NAPHEDDAKÇCASINGVAÇASHASHISNIDHSQP-----WSPCSAYMITSFLDNGHGEC

462

305 VWDPPRPQPGSAGHP---PDAQPGLYYSANEQCRVAFGPKAVACTFARBHLDMCQALSCH 361

463 LMDKPQ-----NPIQLPGDLPGTSYDANRQCQPTFGEDSKHCPDA---ASTCSTLWCT 512 TDPLDQSSCSRLLVPLLDGTECGVEKNCSKGRCRSLVEL---TPIRAVHGRWSSWGPRS 417 S13 GTSGGVLVCQTYCHPPWADGTSCGBGKWCINGKCVNKTDRKCHFDTPF---HGSWGKWGPWG 569 118 PCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLOAEMCNTQAC-EKTQLEFMSQQCART 476 570 DČSRICOGGVQYIMARCDNÝVPKNIGKYCEČKRVRYRSCHIEDČPDNNGKIFRERČC-ZA 628

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548 RVEYRVALTEDRIPELERIRINGPLOEDADIQVYRRYGEBYGNLTRPDITFTYFQPKPRG 707

16.1 ULEPÇPPYWAVGDFGPÇŞASÇGGGLRERPVRÇVEAQGSLLKTLPPARCRAGAQQPAVALE 820

TCNPQPCP 828

32 BW----GECSKSCELG--W------QRRLVECRDING--QPASECAKEVKPASTRPC

---SHE 706

MYKGVULRYSGSSAALERIRSPSPLKEPLTIQUL-----TVGNALRPKIKYTYFVKKKKE 847

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647 774 829

348 RVEYRVALTEDRIPRIEEIRIMGPLQEDADIQVYRRYGEEYGNLTRPDITFTYFQPKPRQ 707 330 SFNAIPTPSAWVIEEW----GECSKSCELG--W------QRRIVECRDING--OPAS 872 754 -----PAWPEACVLEPCPPYWAVGDFGPCSASCGGGLRERPVRCVEAQGSLLKTLPPA 806 973 ECAKEVKPASTRPCADHPC-PQWQLGEWSSCSKTCGKGYKKRSLKCLSHDGGVL---- 925 116 İGRAHIRAH -----TPACHLIGEVQDPELEGGLAAİSACDGLKGVFQLSN-EDYFIE 166 97 RAAGGILH------LELLVAVGPDVPQAH-QEDTERYVLTNINIGAELLRDPSLGAQ 146 227 RPRIRRIHGRSVSKEKMCETLVVADAKOMVEYHGQPQVESYVLTIMD#WAGLFHDPSIGNP 286 147 FRVHLVKAVILITEPEGAPNITANLISSLLSVÇGMSQTINPEDDIDPGHADLVLXITRFDL 206 287 IHITIVRLVLEDBEEDLKITHHADNTLKSPCKWQKSINMKGDAHPLHHDTAILLTRKDL 346 207 ELPDGNR--QVRGVTQLGGACSPTWSCLITEDTGFDLGVTLAHEIGHSFGLEHDGAPGSG 264 347 -CAAMARPOETLGLSHVAGACQPHRSCSINEDTGLPLAFTVAHELGHSFGIQHDGS-GND 404 165 CGPSG---HVMASDGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRPQPGSAGHPPD 321 405 CEPVGKRPFIMSPQLLYDAAPLTWSRCSRQYITRFLDRGWGLCLDDPPAKDIIDF---PS 461 34 SGPREDGTLSLCVSGSCRIFGCDGRMDSQQVWDRCQVCGGDNSTCSPRKGSFTAGRAREX 593 708 -----ANV---WAAVRGPCSVSCGAGLRWVNYSCLDQARKELVETVQCQGSQQP-- 753 17 IGLALLRAMIQRHPRARCPPLC------VAGILACGFLLGCWGPSHFQQSCLQ 62 167 PLDSAPARPGHAOPHVVYKROAPERLAGRGDSSAPSTCGVOVYPELESRRERWEGROOWR 594 VTFLTVTPNLTSVYIANH-----RPLFTHLAVRIG-GRYVVAGKMSISPNTTYPSLLEDG 775 MYKGVVLRYSGSSAALERIRSFSPLKEPLTIQVL----TVGNALRPKIKYTYFVKKKKE 68 ----DST-SVCVQQCCVKAGCDRIIDSKKKFDKCGVCGQNGSTCKKISGSVTSAKP-GY Ouery Match 11.2%; Score 664.5; DB 4; Length 997; DB eff Local Similarity 29.34; Pered No. 2.2e-61; Matches 75; Conservative 94; Mismatches 380; Indels 191; Matches 200; Length 191; Matches 200; L Zinc Metalloproteases PARTICARY New, Sames A PARTICARY Horizontal APPLICARY Historian Science And APPLICARY Historian Science Acids Encoding Zin TILE OF INVESTION NOCIACL ACIDS ENCODING ZINCH MINISTRUM NEW AND ACIDS ACID 807 RCRAGACOPAVALETCNPOPCP 828 ----SHESCDPLKKP 936 Sequence 7, Application US/09369364A Patent No. 6391610 GENERAL INFORMATION: TYPE: PRT ORGANISM: Homo sapiens ADAMTS-7 JS-09-369-364A-7 JS-09-369-364A-7 LENGTH: 997 SEC ID NO 7 g à a ò 셤 à à 윱 g a à 용 à ò è 272 990 NWPHDDAKQCASINGVNQDSHMASMISNIDHSQP-----WSPCSAYMITSFLDNGHGEC 444 362 TDPLDQSSCSRLLVPLLDGTECGVERWCSKGRCRSLVEL----TPIAAVHGRWSSWGPRS 417 118 PCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQAC-EXTQLEFMSQCCART 476 55 DCSRTCGGGVQYTWRECDNPVPKNGGKYCEGKRVRYRSCNLEDCPDNNGKTFREEQC-EA 610 177 DGQPLRSSPGGASFYHWGAAVPHSQGDA---LCRHMCRAIGESFIMKRGDSFLDGTRCMP 533 511 HNEFSKASFGSGPAVEW---IPKYAGVSPKDRCKLICQAKGIGYFFVLQPKVVDGTPCSP 667 83 PPSPGPGRGRG-----RQRRAAGGILHLELLVAVGPDVFQAHQEDTERYVLTNLNIGA 135 136 ELLRDPSLGAGFRVHLVYGVVILTEPEGAPNITANLTSSLLSVCGWSQTINPEDDTDFGHA 195 273 RLYKHESIRNSVSLVVVKILVIHDEQKQPEVTSNAALTLERNFCKWQKQHNPSDRDAEHY 332 .96 DLVLYITRFDLELPDGNR---QVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSF 253 133 DTAILFTRODI --- CGSCTCDTLGMADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVF 389 254 GLEHDGAPG----SGCGPSGHVMAS-----DGAAPRAGLAWSPCSRRQLLSLLSAGRARC 304 305 VMDPPRPQPGSAGHP---PDAQPGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCH 361 145 IMDKPQ-----NPIQEPGDEPGTSYDANRQCQFTPGEDSKHCPDA---ASTCSTLWCT 494 195 GTSGGVLVCQTKHFPWADGTSCGEGKWCINGKCVNKTHRKHFDTPF---HGSWGWWGPWG 551 948 SFNAIPTFSAWVIEEW----GECSKSCELG--W------ORRIVECRDING--OPAS 890 -----PAMPEACVLEPCPPYMAVGDFGPCSASCGGGLRERPVRCVEAGGSLLKTLPPA 806 191 ECAKEVKPASTRPCADHPC-POWQLGEWSSCSKTCGKGYKKRSLKCLSHDGGVL----- 943 213 PQDPALQGVGQPTGTGSIRKKRFVSSHRYVETWLVADQSWAEFHGSGLKHYLLTLFSVAA Query Match
11.84; Score 912; DB 4; Length 949;
Rest Local Similarity 29.74; Pred. No. 2.8e-6.25; Indels 134; Gaps
Matches 239; Conservative 110; Mismatches 320; Indels 134; Gaps WEFLICANT Allact, Dan Application and Applicant Allact, John Applicant Allact, John Applicant Beller, Rent Applicant Beller, Rent Applicant Beller, Rent Applicant Applications Enceling the Same Applicant Applications Enceling the Same Applicant Applications (Applications Enceling Applications Enceling Applications (Applications Enceling Applications Enceling Applications (Applications Applications Enceling Applications (Applications Applications Applications (Applications Applications Applications (Applications Applications Applications Applications (Applications Applications Applications Applications Applications (Applications Applications Applic SEQ ID NOS: 2 FASTSEQ for Windows Version 4.0 307 RCRAGAGQPAVALETCNPQPCP 828 344 -----SHESCDPLIKE 954 Sequence 2, Application US/09568559 Patent No. 6649377 GENERAL INFORMATION: TYPE: PRT ORGANISM: human CENGTH: 949 US-09-568-559-2 18-09-568-559-2 SOFTWARE: SEQ ID NO 2

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Sequence 89, Application US/09800729 Patent No. 6605592 RESULT 12 US-09-800-729-89

GENERAL, INFOMETION: A PARTICANT: Ni et al. APRICANT: Ni et al. TITLE 09 INVENTION: 02 Human secreted proteins FILE REFERENCE: FZO449.
CURRENT PERIOR: PERIOR: ENGINEER 18.09/900,739
CURRENT FILING DATE: 2001-13-08 PRIOR PRIZON NUMBER: PCT/US00/26013 PRIOR PLING DATE: 2000-09-22 PRISON PRICOR TRIADERS: 60/155,709 PRIOR PLING DATE: 1999-024

SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 89 LENGTH: 1745 ORGANISM: Homo sapiens US-09-800-729-89

Indels 257; Gaps Query Match
11.1%; Score 857.5; DB 4; Length 1745; Best Local Similarity 24.6%; Pred No. 18e-60;
Matches 275; Conservative 152; Missaches 434; Indels 257; Matches 154; Jacks 152; Alexaches 434; Indels 257; Alex

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89 RG-----QYKSQLSATKSDDTV-----VAIPYGSRHIRLVLKGPDHLYLET 229 128 -----VAGKWSISPNTTYPSILEDGRVEYRVALTEDRLPRLEEIRIMGPLQEDADIQVYR 682 230 KTLQGTKGENSLSSTGTF--LVDNSSVDFQ-----KPPDKEILRWAGPLTADFIVKI-R 280 88.1 NSGS-----ADSTVQFIFYQPIIHR---WRETDFFPCSATCGGGYQLTSAECYDLRSNRV 332 883 RYGEEYGNLTRPDITFTYFQPKPRQAWVWAAVR-GPCSVSCGAGLRWVNYSCLDQARKRL 741

##GWHTGSCSPKTK--PHIKESCIVPTPCYKPKEKLPVEAKLP--WFKQAQSLSEGAAVS 504 ---RTGAQAAHVWT 921 505 BEPSFIPKAWSACTVTCGVGTQVRIVRCQVLLSF8QSVADLPIDBCBGFKPASQRACYAG 564 322 PAAG-----SCSVSCGRGINELRFLCMDSALRV 949 902 KAPS----PWGSI-----

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95 GVHYEYTIHREAGGHDEVPPPVFSWHYGPWTKCTVTCGRGEKWGRHSPT-CRGLVSGQGH 953

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068 GQDVEVDENACAALVRPEASVPCLIADCTYRWHVGTWMECSVSCGDGIQRRRDTC---LG 1124 945 GSFLELPETFCSA-SKPACOGACKKDDCPSEWLLSDWTECSTSCGEGTGTRSALCRRMLK 803 g 8 a

125 PGAGAPVPADFCQHLPKPVTVRGCWAGPCVGQGTPSL--VPHEEAA-----APGRITATP 1177 904 TGLSTVVNSTLCPPLPPSSIRPCMLATCARPGRPSTKHSPHIAAARKVYIQTRRQRKLH 863 유

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883 NFVPKNGGKYCEGKRVRYRSCHLEDCPDNNGKTFREEQC-EAHNEFSKRSFGSGPAVEW- 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 KAGCDRIIDSKKKPDKCGVCGGNGSTCKKISGSVTSAKP-GYHDIITIPIGATNIEVKQR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----RPLFTHLAVRIG-GRYVVAGKMSISPNTTYPSLLEDGRVEYRVALTEDRLPRLEE 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 NORGSRNNGSFLAIKAADGTYILNGDYTLS-----TLBQDIMYKGVVLRYSGSSAALER 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRIMGPLQEDADIQVYRRYGEEYGNLTRPDITFTYFQPKPRQ------AWV---WAA 713
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SELCANT GOODERS INGOORD TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
TITLE OF INSERTION INSERT.
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Sequence 13, Application US/09130491
Patent No. 6416974
GENERAL INFORMATION:
                                                                                                                838 SCISAGGAGLALENETCV 855
                                                                                                                                                                                                                                347 ECSRSCDGGTHRRRAICV 864
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10.5; Score 813; DB 4; Length 874;
Best Local Similarity 27.8; Pred; No. 2.8e-57;
Matches 222; Conservative 113; Mismatches 347; Indels 114;
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                      US-09-369-364A-15
; Sequence 15. Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
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US-09-369-364A-15
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664 BEIRINGPLOEDADIQVY---RRYGEBYG---NLTRP-----DITFTYFOPKPRQAWWA 71.2
593 HIEVREVAMSKNYIALKSEGDDYYINGAWTID----WPRKFDVAGTAFHYKRPTDEPESL 648
                                                                                                                                                                                                       649 EAL---GPTSENLIVWVLLQBQNLGIRYKFNVPITHTGSGDNEVGFTW----NHQPW--- 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 RLIVLTEDQ--PNLEINHHADKSLDSFCKWQKSİLSHQSDGNTIPENGIAHHDMAVLITR 207
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10.0%; Score 776; DB 4; Length 757;
Met Local Similarity 29,9; Fred, No. 2.1e-54; Indels 108; Gaps Matches 213; Conservative 108; Mismatches 283; Indels 108; Gaps
                                                                                                                                                     559 -- GECSKIOGKGYKKRSLKCLSHDGGVIGHE-SCDPLKKPKHFIDFCINARC 607
                                                                          714 VRGPCSVSOGAGLRWVNYSCLDQARKELVETVQCQGSQQPPAWPEACVLEPC 765
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CURRENT FILTION DATE: 5000-12-69
PRIOR ELECTRON WINGER: 108/09/169,769
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) Sequence 24, Application US/09963791
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Copyright (31.599 - 2004 Compugen Ltd. OM protein - protein search, using aw model Run on: March 13, 2004, 07,131.9; Search Ltme 3,1849 Seconds Firite: 108-09-86-712-2_COPY97	Cearched: 23356 eeqs, 9519152 residues Total number of his satisfying chosen parameters: 283366 Mostimum D seq longht; 0 00000000 Maximum D seq longht; 0 00000000 Post-processing Mostimum Meth On Post-processing Acada Noor	se : Pred. No. score grea	National

A, Molecule type: DWA A.Gene: SPBC646.01c

A.Map position: 2 C.Superfamily: yeast TOR2 protein

Query Match Best Local Similarity

Matches

1196 TSPHISP 1202

69 VSSYLSP 75

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Depotestion) process aliang (imported) - Nostoc sp. (strain PCC 7120)
Appetestion process aliang (imported) - Nostoc sp. (strain PCC 7120)
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A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                             C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 13-Aug-1999
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C;Superfamily: gap junction protein
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illarity 30.0%; Pred. No. 8.1;
Conservative 6; Mismatches 27; Indels
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C.Keywords: ATP
Page 19.1168/Domain: discoidin I amino-terminal homology «DNI»
F.665-909/Domain: protein Kinase homology «KIN»
F.613-621/Region: protein Kinase ATP-binding motif
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Best Local Similarity 29.6%;
Matches 29; Conservative
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Best Local Similarity
Matches 21, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-402 <GUP>
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Radite, E. 143, -7. A.
Radite, E. 143, -7. A.
Radite, Endishing of the receptor typosine kinase gene P.E.3 in normal rat.
A.Retenence number; 18442; WIID-8532023; PMID:1857135
                                                                                                                                                                                 AlResidues: 1-396 -688.
Alcross-cetences: RNBL-ALGASZIE, PIDN:CAAZ2805.1; GSPDB:GN0067; SPDB:SPBC646.01c
AlEXPEX:mental sources strain 972h-, cosmid c646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1137 LGVALLRESPSHALRACAALAAAYQPLARDLFNASF-VSCWSELYDHFQEELVKSIETAL 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 PYGEPRPRGTPTHSAPCVPNGSALLLSNPAYRLLLATYARPPRGPGPP----- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 LGLALLRAMORHPRARCPPLCVA-----GILACGFLLGCWGP--SHFQQSCLQALBPQA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PGRPTRPK-APSHSAPLL--GLA------LLRMHQRHPRARCPPLCVAGILACGFL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.Species: Rattus sp. (rat)
0.Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 14.0t, Score 74.5; DB 2; Length 2337; L Similarity 29.9t, Pered. No. 23; DB 20; Indels 9 9.0; Conservative 10; Mismatches 28; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.9%; Score 74; DB 2; Length 220; 29.6%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 LGCWG-PSHFQQSCLQALEPQAVSSYLSPGAPLKGRPP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Status: preliminary, translated from GB/EMBL/DDBJ A:Molecule type: mRNA
                   preliminary, translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor tyrosine kinase - rat (fragment)
```

29; Conservative

Local Similarity

A,Residues: 1-220 <RES>

A:Gene: Ptk-3L

tyrosine kinase receptor - rat

RESULT 4

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Cipression 18550

Proc. Mark. And. Std. 10.5. Ag. 65.65611 1893

Applicate number: Acetage number: Acetage number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number number 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: AE002019; GB: AE000513; NID: 96459547; PIDN: AAF11334.1; PID: 96459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclession B7553
Rintio Co. State, John Heidelberg, Jr.; Hickey, R.K.; Peterson, J.D.; Dodon, R.J.
K.; Shen, M.; Manthwan, J.J.; Lida, P.; McDonald, L.; Uterlands, T.; Zalewski, C.;
S.; Salki, M.; Wanthwan, J.C.; Frener, C.K.
S.; Salki, M.; Wanthwan, J.C.; Frener, C.K.
S.; Salki, M.; Wanthwan, J.C.; Frener, C.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. Firle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A. Reference number: A75250; WJID: 20036896; PMID: 10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                439 PGRGRRTAKSSANDLPASDI-----FASEPPARCPPODNLOSRSRTSWISSKAMILDQWG 493
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    PGRPTR-PKAPSHSAPLLGLALLRAHORHPRARCPP-----LCVAGILACGFLLGCWG 52

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C.)Speciae: Deinococcus radiodurans
C.)Speciae: 03-Der-1999 #sentoccus radioduranse. Per 03-Dec-1999 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 24-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.2%; Score 70.5; DB 2; Length 135; 25.5%; Pred. No. 4.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 24; Conservative 11; Mismatches 30; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 PYQEPRPRGNPPHSAPCVPNGSALLLSNPAYRLLLATYARPPRGPGPP-
                                                                                                                                                                                                                                                                           494 P-FVGLGTVPVTPPQAGPWTPVVXSPSTTVVPGALISGQPPS 534
                                                                                                                                                                                                           53 PSHFQQSCLQALBPQA-----VSSYLSPGAPLKGRPPS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-185/Domain: discoidin I amino-terminal homology <DN1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 LGCWG-PSHFQQSCLQALEPQAVSSYLSPGAPLKGRPP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F,608-912/Domain: protein kinase homology <KIN>
F,616-624/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches
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Best Local Similarity 29.6%; Pred. No.
Matches 29, Conservative 8; Kismarr
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A; Residues: 1-135 <WHI>
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SYNL SA, Y. Mang, W. (J. Sackowski, S.) ROCK, C.O.

ATTILLS (C) CONTROL OF A LOVEL PROPROPORTORIES (MARCHEST) COLOMY-stimulating factor 1 sheat

A. Reference complex in ASTACLA (MID.95284008) FANDATSAT79
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                                                                          299 HPRRRRQP------GPARRQNWANREAEPQTSSRKASPPAPTRLQPRAPG 342
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          28 HPRARCPPLCVAGILACGFLLGCWGPSHFQQSCLQALEPQAVSSYLSFGAPLKGRPPSFG 87
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C.pate: 23-Feb-1396 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996
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A; Note: authors translated the codon GCT for residue 789 as Thr
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13.4%; Score 71.5; DB 2;
Best Local Similarity 28.4%; Pred. No. 18;
Best Local Similarity 28.4%; Pred. No. 18;
Stational 29; Conservative 11; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                      343 VAPSSPFRRR 352
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A.Molecule type: DNA
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A:Molecule type: mRNA
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A57542

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13 GRRIKASAPARESHSSGKATVKEKGR----RCHPALVAAAOADGM-

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62 QALEPQAVSSYLSPGAPLKGRPPSPGFQ-RQRQR

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Ryanthews L. 2.; Vala, W.H.
(16, 57)-258-200 c. long of an activin receptor, a predicted transmembrana serine k
A.7151e. Spresse. On Cloning of an activin receptor, a predicted transmembrana serine k
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                                                                                                                                                                                                                                             C.Species: Mus musculus (house mouse)
C.Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 18-Jun-1999
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:/Residues 1_513 cARTS
;/CROSSES=Reference: 2MSLX63128; NID:g3928172; PIDN:CAA44839.1; PID:g28350
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Prigo-56/Region: protein kinase AFP-binding motif
Prigo-56/Region: protein kinase AFP-binding motif
Prigo-56/Region: protein kinase AFP-binding motif
Prigo-56/Region: acarbohydrate (Asn) (covalent) #status predicted
Prigo-78/Active sites: Lys #status predicted
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submitted to the EMBL Data Library, December 1991
A;Reference number: 518908
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R;Geiser, A.G.
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A, Residues: 1-513 <DON>
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PGCPQSWRRMPSSCPALA-----RHPSPSSQCWRRMKRSRCPGSPITAQRPVASPLW 694
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A)A)Cross-raferences: BMBL:US2917; NID:g1279850; PID:g1279872; PIDN:AAA97949.1
A)Experimental sources: strain HB-8
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C/Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 05-Nov-1999
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Indels 17;

DB 2; Length 606;

Superfamily: NADH dehydrogenase (ubiquinone) chain 5 Keywords: membrane-associated complex; NAD; oxidoreductase

A, Gene: NQ012 Genetics:

A,Accession: T11909 A/Status: preliminary, translated from GB/EMBL/DDBJ A/Rolecule type: DNA

Natch 13.2%; Score 70.5; DB 2; Local Similarity 30.9%; Pred. No. 17; es 21; Conservative 7; Mismatches 23;

Query Match Best Local S: Matches 21

71 SYLSPGAP 78 61 ---- PGIP 64

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B38252

25.

13.2%; Score 70.5; DB 2; Length 771; 23.3%; Pred. No. 21; 11ve 8; Mismatches 39; Indels 59

31; Conservative

Query Match

A:Residues: 1-771 <FUK> Local Similarity

A,Status: preliminary A,Molecule type: mRNA

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Abdetereme maker, A38956, MID:91286317, PMID:1646500
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C) Received N. 4939.

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172 LVPTQ----DPGpP----PPSP 185

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Search completed: March 13, 2004, 07:44:38 Job time : 5.3849 secs

172 LVPTQ-----DPGPP----PPSP 185

4 PTRPKAPSHSAPLIGLALLRAHORHPRARCPELCVAGILACGFLLGCWGPSHFOOSCLOA 63

Score 70; DB 2; Length 513; Pred. No. 16; 7; Mismatches 27; Indels

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MEDINIB-56136713; PubMed-2557189;
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Genes Dev. 10:103-117(1996).
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32, Gaps 14.0%; Score 75; DB 1; Length 958; 26.8%; Pred. No. 7.6; 15, Mismatches 35, Indels Conservative Best Local Similarity Matches 30, Conserv Query Match

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This STRESS POT Entry is copyright. It is produced through a collaboration between the State Institute of Biothformatics and the BEW outsetton. The Broppean collisions in this time, where are no restrictions on its the Broppean collisions in the time is made are serviced. The state of the s

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Score 74; DB 1; Length 910;
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MEDLINE-22388257; PubMed=12477932;
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Matches 29, Conservative
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                                                                                                                              9; Gaps
                                       DB 1; Length 2337;
                             Onery Match
14.04; Score 74.5; DB 1; Length 233'
est Local Similarity 29.94; Pref. NO. 20;
Macches 20; Conservative 10; Mismatches 28; Indels
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Gaps

4 PLPPPSPRHLRLLRLLLSGLVLGAALRGAAAGHPDVAACPGSLDCALKRRARCPP----G 59

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This BYESS POT entry is experight. It is produced through a collidoration between the Bases institute of Basinformatics and the BRES collection of Basinformatic in the European Boofficerstein Entities. There are no restrictions on Its modified and thus extended to the record, the accordance of the extended to the recorded. Uses to Moral for commercial entities extract a literature assembled agreement (see http://www.isb-sib.ch/announce/or seed an earli to incommercial the produced an earli to incommercial the second of seed and second of seed and second of seed an earli to incommercial the second of seed an earli to incommercial the second of seed and second of seed and second of seed and second of seed and second of seed and second of seed and second of seed and second of seed and second of seed and second of seed and second of second of seed and second of seed and second of seed and second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of second of 
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PRO/SER/THR-RICH.
H -> Q (IN REF. 1).
C -> M (IN REF. 1).
Q -> H (IN REF. 1).
KADAWANAA -> BSRLANCBC (IN REF. 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches 33, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evrard C., Apiou F., Dutrillaux B., Rouget P., Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E -> D (IN REF. 4).
21D6512AD345A575 CRC64;
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ENEL, AF2237 AF47225, 1 --
ENEL, AF2327, AAF8260.1 --
ENEL, AC08021, CA843321.1 --
P.R. TO8809, T08809
MMK, 660798, --
MKK, 660798, --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF285836; AAK27328.1; -.
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Best Local Similarity 26.8<sup>†</sup>
Matches 30; Conservative
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12.808-2007 (Rel. 46. Last seaturetten update)
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WEDLINES-DOUGHES, DEMMORA-201107,
WEDLINES-DOUGHES, DEMMORA-201107,
WEDNINGS, MICHAEL PE, MINCH MA. FREIN, MARCHEN M.-G.,
WESTER, M. MICHAELON, CON CHARTOGAINE MISSES GENE RESPONSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. Popurior May be interested in call-call interactions and control may be interested on call-call interactions and control may be interested in call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call of the call 
41 ILACGFLIGCWGPSHFQQSCLQALEPQAVSSYLSPGAPLKGRPPSPGFQRQR 92
                                                                                                                                   60 AHACG-----PCLOPFORDQGLCV----PRMRRPPGGGRPQPR 94
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Name=1; Synonyms=CAK I;
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MGD; MG1:99216, Ddr1.
InterPro; IPR00421; PA58 C.
InterPro; IPR008979; Gal Dind like.
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Q03146;
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1 PGRPTRPK-APSHSAPLL--GLA------LLRMHQRHPRARCPPLCVAGILACGFL 47
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Memalia Balhetis; Cetartiodactyja; Rumisantia; Pecora; Bovoidės;
NEE Tartio-9940;
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0.-807-197 (Rel. 35, Last sequence update)
13-MAR-2004 (Rel. 43, Last amoutation update)
Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
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19-MAR-2004 (Rel. 43, Last aumotation update)
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Mammalia, Burheria, Primates; Catarrhini; Hominidae; Homo.
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185 R >> 0 (IN REF. 1, BAB71493).
189 189 R >> W (IN REF. 1, BAB71493).
274 AA, 30081 MM, EDB20002E426E81A CRC64;
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F5/8 TYPE C.
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InterPro; IPROG642; DUF_DM3.
Pfam; PF05485; THAPP. 1.
SMART; SK00692; DM3: 1.
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"Molecular cloning and binding properties of the human type II
activian receptor.";
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Mean, General 1869-861-9867.

- Thorrios: Reseptor for activin A, activin B and inhibit A.

- Thorrios: Reseptor for activin A, activin B and inhibit A.

- Thorrios: Activity: ARV = grotein = ADP = a phosphoprotein.

All ACTIVITY: ARV = grotein = ADP = a phosphoprotein.

ATM = ACTIVITY: ARV = grotein = ADP = a phosphoprotein.

- STRIAMINION = ADP = and ADMANI = Parillativity consisting of experience and ADMANI = and ADMANI = activity of protein kinases. TGDB = acception and ADMANI = and ADMANI = acceptor and and ADMANI = acceptor and activity = acceptor and and administry.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae: Bovinae: Bos.

NCBI_TaxID=9913;

SECUENCE FROM N.A.

Bos taurus (Bovine).

STRAIN-Holisedii, TISSUB-Testis; MEDLINE-9520347; Pubbde-753470; Ebbrar J.F. Houde A., Lussier J.G., Silversides D.W.; Ebvine activin receptor type II cDNN: cloning and tissue

. Cell. Endocrinol. 106:1-8(1994) TISSUE=Ovary; MEDLINE=97032546; PubMed=8875905;

expression.";

SECUENCE FROM N.A.

Monteagudo L.V., Heriz A., Flavin N., Rogers M., Ennis S.,

Arruga M.V.;

EMBL; L21717; AAA74597.1; -. EMBL; U43208; AAC48694.1; -. PIR; 145850; 145850.

01-NOV-1997 (Rel. 35, last sequence update)
15-MR-2004 (Rel. 43, last amootation update)
Activin receptor type II precursor (SC 2.7.1.37) (ACTR-II).
ACVR2 OR ACTRII.

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STANDARD;

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BRBL; X6228; CAA4424.1; -.
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Greenwald J., Flether M. H., Yala M. W. Choo S.,
Three-finger coxin fold for the extracellular ligand-binding domain
the type II activin respons seatine Kinase.';
NR., Struct. Biol. 6;18–22(1999).
                                 Gaps
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MARANNER H., Tutchida K., Kilehi H., Yamakawa N., Matsuzaki T., Liu Z.,
Makamura T., Sugino A. Kilehi H., Yamakawa N., Matsuzaki T., Liu Z.,
Nidekni H., Sugino And Characterization of a POZ protein that Interacts
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Fischer W.H. Greenwald O., Park M., Craig A.G., Choe S., Vale W.,
The disulfide bode arxangement in the extracellular domain of the
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                 27; Indels 26;
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01-AVG-1992 (Rel. 24, Lest sequence update)
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J. Protein Chem. 18:437-446(1999).
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MEDLINE=91256317; PubMed=1646080;
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Cell 65:973-982(1991).
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129 PVTPKPPYYNILLYSLV-------PLMLIAGIVICAF----WVZRHHKMAYPPV 171
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                                                                                                         ACTIVIN RECEPTOR TYPE II. 
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MBL, M65287; AAA37171.1;
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33.3%; Pred. No. 0.14;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muxidae; Murinae; Mus.
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Tharacterization of nove bHIM genes.", DBJ databases.
"Characterization" to the bHIM Genhank, DDBJ databases.
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PROSITE; PROGOSS; HLH; 1.

PROSITE; PSGORGS HLH; 1.

SEQUENCE; PSGORGS HLH; 2. 1.

SEQUENCE; 2550888 HLH; 2. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 AA; 24899 NW; 4B22E7D4D57FF5E8 CRC64;
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01-JUN-2001 (TERMELTEL 17,
01-JUN-2001 (TERMELTEL 17,
01-OCT-2003 (TERMELTEL 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAM, PF00010; HLH; 1.
SMART, SM00353; HLH; 1.
PROSITE; PS00038; HLH 1; 1.
PROSITE; PS50888; HLH 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 33.39
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099JA6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 MHQRHPRARCPPLCVAGILACGFLLGCWGPSHFQQSCLQALBPQAVSSYLSPGAPLKGRP 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MEGREPRARCEPLICAGILACGFLIGCWGPSHFQQSCLQALRPQAVSSYLSPGAPLKGRP 60
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                                 75 1427 VON WILLEBRAND FACTOR-CLEAVING PROTEASE 1427 AA; 153632 NW; BB1BC3AABC1A4442 CRC64;
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Mammalia, Butheria, Primates, Catarrini; Hominide, Homo.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                              177.5%; Score 414; DB 4; Length 1427;
100.0%; Pred, No. 2.3e-37;
iive 0; Mismatches 0; Indels
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PROSITE: PS00039; HIM; 1.

PROSITE: PS00898; HIM; 1.

SEQUENCE: 2550889; HIM; 2. 1.

SEQUENCE: 2558889; HW; 02785BAAB4ACB247 CRC64;
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OBENTA, OR TERMELS, 17, Created B.

OBENTA, OR TERMELS, 17, Created B.

DELONGON, OR TERMELS, 17, Created B.

DELONGON, OR TERMELS, 17, Last mequance update)

BENTA GREEN B.

HEST. L. 25, LAST MICROST MARKET, 185, LAST                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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Last sequence update)
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Genera, MGNC 11697; HESG.
OO GOODGSS94; CINCACLERS, NA.
OO; GOODGS94; FINNA BIRGHING NA.
OO; GOODGS97; FINNA BIRGHING NA.
THE CONTROL OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STA
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01-WAR-2003 (TERMBLEEL 23,
01-OCT-2003 (TERMBLEEL 25,
BHLM factor MB97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 PSPGFORORORR 97
                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PSPGFORORORR 74
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                                                                                                                      SEQUENCE
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SOUND BRANCH THE SOUND

OBBKT2

88844448

RESULT 3 QBBKT2

41; Gabs

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309 RPVPPPARLAYYAAVG-GHIRFHRRQPRSPLTGVIACTASILCRRCWASTSSPPACLRLL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 PIGVLACTAGLLCRRCWASISSRPACLCRRRPVPPPAPLAYYAAVVRCIRLSPPACLCRR 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RPTRPKAPSHSAPLIGLALLRMGRHPRA-------RC-----Pplcv--- 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 -AGILAC--GFLL-GCWGPSHFQQSCL---QALEPQAVSSY-----LSPGAPLKGR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 GRERIHRREASVAAEWCLRLHGWSIMPELLGV-----HDFTAGLPPLPPSGASAYTA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GRFTRPKAPSHSA-------PLLGLALLRNHQRHP-RARCPPLCVAGILA--C 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Onyza sativa (japonica onlitvar-gota).
Parantopta, Viridajlantae, Streptophyta zmbryophyta; Tracheophyta;
Sprantophyta nagnoiclophyta; Lillopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 1187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAINA-W. Mipponhaise;
**Rice Chicomsone in Sequencing Consortium;
**In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.3%; Score 81.5; DB 10; Length 649;
28.8%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAINCH Nigorach, Nacombie W.R., Messing J., Yuan O.; Bubli C.R., Ming R.A., McCombie W.R., Messing J., Yuan O.; Submitteed (MAY-2003) to the RNBL/MenBank/DoBJ darabases. PRUBL, MED1710, AAP$4044.1; -.. PRUBL, MED1710, AAP$4044.1; -.. RSDDBMCE 649 AA, 71149 MN; REREA22805DCD778 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Indels
                                                                                                                                                                                                                                                                                     130328 MW; EDC8A0AA4A7CC920 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                         Score 82.5;
Pred. No. 1.
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                      EMBL: AP001389; BAA92718.1;
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                                                                  Gramene, O9LWUZ; --
InterPro, IPR005213; HGWP.
Pfam; PF03578; HGWP; 9.
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SEQUENCE 1187 AA;
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                                                                                                                                                           1 PGRPTRPKAP-SHSAPLLGLALLRMHQRHPRARCPPLCVAGILACGFLLGCWGPSHFQCS 59
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                                                                  23; Gaps
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Spermatophyta, Magnollophyta, Liliopaida, Poales; Poaceae;
Enthatroideae, Oryzeae; Oryza,
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15.4%; Score 82.5; DB 10; Length 281;
Best Local Similarity 28.8%; Peted. No. 0.58;
Matches 36; Conservative 7; Mismatches 39; Indels 43;
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Sasaki I. Warmoto T. Yamanoto X., Sasaki I. Warmoto T. Yamanoto X., Chromosome 6, PAC ("Orysa mattyrn imprombere(GAS) genomic DNA, chromosome 6, PAC ("Orysa mattyrn imprombere(GAS) genomic DNA, Chromosome 6, PAC ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) genomic CAMP ("Organ patha) geno
                                                                  6; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 AGDSGAPAPLTGLLPPPPPPYRGDGAPKAPPLPPPAPWR 222
                                                                                                                                                                                                                                                                                                                                                                              60 C-----LOALEPOAVSSYLSPGAPLKGRPPSFGFQR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-007-2000 (TrabBizea, 1s, Created)
01-007-2000 (TrabBizea, 1s, Lear sequence update)
01-007-2002 (TrabBizea, 2s, Lear annotation update)
Myponebectal procesa.
05.pss setive (Rice).
           33.3%; Pred. No. 0.17;
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                                                       33; Conservative
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Best Local Similarity
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         RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 RPVLPGAEPVPLAAAPVPGLS----QRHPPARCR----AG-LHGSLPAGCHVPPVHRGV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGRFTRPKAPSHSAPLLGLA----LLRMHQRHPRARCP-PLCVAGILACGFLLGCWGPS 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 PSHPQQSCLQALEPQAVSSYLSPGAPLK------GRPP-SPG 87
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01.-WAR-2001 (TERMILE). 16, Last sequence update)
01.-WAR-2001 (TERMILE). 23, Last amoration update)
01.-WAR-2001 (TERMILE). 23, Last amoration update)
WAR-2017.11 (Novel procein familiar to artic finger procein human
mannodeficiency virus type I enhancer-binding procein 1 (HIVBPL))
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Kammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.2%; Score 81; DB 4; Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Variabing W. A. Addition to the BMBL/GenBank/DDBJ databases. Submitted (REP-2011) to the BMBL/GenBank/DDBJ databases. Bypotherical protein. AMBL 333.1.1 - Bypotherical protein. SEQUENCE 259 AA; 26945 VM; PS94FCEA861CCBC7 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Similar to hypothetical protein FLJ11467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPOGSCLQALEPQAVSSYLSP--GAPLKGRP---PSPG 87
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MEMBER, MANUEL ST, CACATOSTO 11.

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TISSUE=Lung;
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44 PGIHEQPPQASHSRPINGLIRIGIPGDWYARSEPFARGPWARSDTLATAIH-GYGGWN 102
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"Nailysis of the mouse transcriptome based on functional annotation of 60.770 fill.11-sept. ORMs."

Nature 420:555-573 (2002).

BREIL, MOSSEGE, BGCS233-11.
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From It is come to make translatione based on functional annotation of 

Makers 401:65-573100021.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
"Lax.Dat.090"
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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27.9%; Pred. No. 0.69;
tive 12; Mismatches 49; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
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STRAINS-ESTBL/61, TISSUB=Cerebellum, and Head,
MEDITNE-22394683; PubMed=12466851,
The FANTOM CORRECTION.
249 AA
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                                                                                                          the derebellum 4
                                              Created)
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InterPro; IRR007087; Znf CZH2.
Pfam; PR00096; Zf CZH2, J.
ProDoom; PD000003; Znf CZH2, 1.
                                     01-WAR-2003 (TrENBLrel. 23,
01-WAR-2003 (TrENBLrel. 23,
01-OCT-2003 (TrENBLrel. 25,
Zinc finger protein of the
ZIC4.
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PRELIMINARY;
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                                                                                                                                                         Mus musculus (Mouse)
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Best Local Similarity
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1 PGRPTRPKAPSHSAPLLGLALLRMHQRH----PRARCPPLCVAGILACGFLLGCWGPSHF 56
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Picklenhand, D. Alladon, Elsen J.A., Carpenter L., White O.,
Picklenhand, D., Alladon, Elsen J.A., Carpenter L., White O.,
Petergon J., Pelloy R., Doddon R., Oainn M.L., Batt D., Hickey E.,
Colony U.F., Palion M.C., Howpen L.A., Emchaeve M.D., Silzberg S.L.,
Picklenhand A., Utterback T., Weidman J., Kfourt H., Vill J., Wikhla A.,
Picklenhand R., Weidman J., Kfourt H., Vill J., Wikhla A.,
                                                         Eukaryota: Metazoa; Chordata; Cramiata: Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peals F.V. 2. Macon X. Hunter A.M., Southerl M., Statistics and resolves 
Wittinghard display polymerase chain resoltion ampliffies and resolves 
related sequences histing a single moderately conserved domain."; 
Ambl. Sicolem. 256:128-168(1998).
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Basteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Copynabacterines; Mycobacteriacses; Mycobacterium.
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28.3%; Pred. No. 0.98;
ive 2; Mismatches 31; Indels
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OJ-WAR-2002 (TEBMBLTEL: 20, Last Sequence update)
OJ-027-2003 (TEBMBLTEL: 25, Last annotation update)
Mypothetical protein MT0291.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS0071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
VARIANT 154 154 154 P -> S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001356; Homeobox.
InterPro; IPR007104; Paired homeo.
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MEDLINE=98141813; Pubmed=9473273;
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ProDom; PD000010; Homeobox; 1.
SMART; SM0389; HOX; 1.
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                   Sallus gallus (Chicken).
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                                                                                                                                                        Gallus.
NCBI_TaxID=9031,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PGRPTRPKAPSHSAPLLGLALL----RMHORH-----PRARCPPLCVAGILACGF---- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 RPKAPSHSAPLLGLA----LLRMHQRHPR-----ARCPPLCVAGILACGPLLGC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RKDBTSNTSPDISVAQPASALRYHLRPPRRNDGAAIHQLVSBCPPLDLNSLYA--YLLLC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINISTRATISTS, DARLISH W. PERGORA. NEEPHY LO. THORSEN N. .

DEFINITION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 LTMMLTAPHGPGAPPRYMRQPIKOELICKWLGDDSPMSPRPCSKTPSTMHE 160
                                                                                                                                                                                                                                                                                                                                              49; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 ---- LLGCWGPSHPQQSCLQALEPQAVSSYLSPGAPLKGRPPSPGPQRQRQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella parapertussis.
Bacceria: Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenacea; Bordetella.
NCBL TaxiD=519;
                                                                                                                                                                                                                                              14.9%; Score 79.5; DB 11; Length 341;
27.9%; Pred. No. 0.94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  il.OCT.-2003 (TERMILE). 25, Created)
10-OCT.-2003 (TERMILE). 25, Lage sequence update)
10-OCT.-2003 (TERMILE). 25, Lage annotation update)
10-OCT.-2004 (Manuschitz) (Manuschitz) (Manuschitz)
10-OCT. 908 BPP1888.
SWART; SMO0355; ZAF_C2H2, 5.
PROSITE: PRODO22; ZINC FINER_C2H2_1, 3.
PROSITE: PSSG157; ZINC FINER_C2H2_2, 4.
SRQUENCE .341 AA, 37437 WM; B48BIODE736230CF CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRI, Genet. 35:12-40(2003).
NRIBLI, BX640428; CAB37189-11;
ACA/LTAINSERSARS, TATARRETARS, COMPLETE protecme.
SEQUENCE 186 AA, 20729 WW; C037071691790F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 --- EHHAHTCVVAESPGGRIDGFVSAYLLPTRP 89
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; Pred. No. 0.68;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .68:
                                                                                                                                                                                                                                                                                                                                     31; Conservative 12; Mismatches
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01-AUG-1998 (TERBLES). 07,
01-MAY-1999 (TERBLES). 10,
01-JUN-2003 (TERBLES). 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.1%;
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Matches 31; Conserv
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AC 073592
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SWELFFERENCES

Search completed: March 13, 2004, 07:43:19 Job time: 12:599 secs

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                  921 ----HTDSSCMLTPPSTPLGLEPAGPSWPEPSGLCGRAVLDGQRWGPGGLPGAVLEGDAI 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 PSPPSAPVAPWPDLPPLPRNHPPAPPSAPVPGVPLAPLPISGRPVRAWVGSLIALRICCC 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PGRPTRPKAP----SH----SAPLLG--LALLRMHQRHPRARCPPLCVAGILAC 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 ----GFLLGCWGPSHFQQSC-----79
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                                                                                                                                                                                                                                                                                                                                                                                                                                          14.5%; Score 77.5; DB 16; Length 598;
28.6%; Pred, No. 2.7;
tive 7; Mismatches 40; Indels 47; Gaps
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0.1007-1803-2030 (TEDBRIDGE, 2.5, Late sequence update)
0.1007-2030 (TEDBRIDGE, 2.5, Late amortation update)
Mycothetical Gram-possitive cocci surface protein 'anchoring'
hakappostide/RA domain/PDZ domain.
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. BRBLL, RSD06377 ARX44515.1; "If the RYPOTHET CAST PROPERTY OF SUBJECT PROPERTY OF SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUBJECT PROPERTY SUB
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SECURNCE 992 AA; 108964 MW; 13AB2678AB9BE1FC CRC64;
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Best Local Similarity 27.2*
Matches 37, Conservative
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Best Local Similarity 28.83
Matches 38, Conservative
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Pfam, PF00788; RA, 1.
SMART, SM0314, RA, 1.
PROSITE, PS50200, RA, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleoride, useful in gene therapy, particularly for treating or preventing e.g. arthritis, Conford disease, Altheimer & disease and organ transplant poxydicty and redection, comprises ADMYTS polynucleoride and
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extracellular matrix interaction; tumour suppression; game maturation;
mamunologic recognition; gastrointestinal irradiation; chemocherapy;
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larity 100.0%; Pred. No. 1.6e-46;
Conservative 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                   Wachtmann TS. Walsh RT;
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27-APR-2000; 2000US-0200040P.
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                                                                                                                       (PFIZ ) PFIZER PROD INC
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N-PSDB; ABA02549.
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es 97; Conserv
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cell fusion; cell signalling; tumour; Crohn's disease; melanoms; trauma;
inflammatory bovel disease; Cod poisoning; desponsative disease;
riflammator; fertility; gamete maturation; opithelial disorder.
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                                                                                                                                                                                                                                                                                                            'note= "unspecified residue encoded by TTN"
                                                                                                                                                        Location/Qualifiers
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                                                                                                              Homo sapiens
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| RAPSHSAPLIGIALIRWHQRHPRARCPPLCVAGILACGFLIGCWGPSHFQQSCLQALEFQ

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Indels

Length 1120;

92.1%; Score 492; DB 4; I 100.0%; Pred. No. 2.9e-42; 100.0%; Pred. mc.

90; Conservative

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Local Similarity

Query Match Matches

9

Gaps

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and meralopproses (Asob), the gene for hitch is located on human meralopproses (Asob), the gene for hitch is located on human Changesen (Asob), the gene for hitch is located on human Changesen (Asob), the gene for hitch is located on human changes (Asob), the gene for hitch is located on human changes (Asob), the gene for hitch is located to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid to the hitch is located asobid 
15 KAPSHSAPLIGIALLRWHQRHPRARCPPLCVAGILACGFLLGCWGPSHFQQSCLQALBPQ 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Minaan; alizin; ANAN; a distingent mad mealingonesse; deergent; home defence; unour; extracellular matrix repair; proceolysis; apoproass; anglogenseis; becrearid infection; Crohn's cleasee; inflammonous; Deeb Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
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                                                                                                                                                         75 AVSSYLSPGAPLKGRPPSPGFQRQRQRQRR 104
                                                                            68 AVSSYLSPGAPLKGRPPSFGFQRQRQRR 97
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                                                                                                                                                                                                                                                                                                                                                                       ABG74113 standard; protein; 1120 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label UNKNOWN
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(SHEP/) SHEPPARD P O.
(YAMA/) YAMANOTO G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 1118.
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the superpers animal, immunisation; thromboembolic disease; presclampela, 
thrombolic thromboric purpures, TTP; Penond-Schoolarn purpurs; 
thrombosis, encoural introdocyposania, incompose, and presents syndrome; 
transpenic; anticoagulant; chromosome 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                        8 KAPSHSAPLIGLALLRMHQRHPRARCPPLCVAGILACGFLLGCWGPSHFQQSCLQALBPQ
                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                           92.1%; Score 492; DB 6; Length 1120;
100.0%; Pred. No. 2.9e-42;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Von Willebrand factor-cleaving protease (vWF-cp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mature human vWF-cp protein"
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Best Local Similarity
                                                                                                                                                                                                                                                                                                           Sequence 1120 AA;
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'note= "Thromspondin type I motif"

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Domain.

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processe, useful for producing preparation for threapy of thrombosis and 
htrombosinglis disease such as thrombosis chrombosytic purpurs.
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r P, Antoine G, Kerschbaumer R, Tagliavacca L;
"Thromspondin type I motif"
                                                                                    'note= "Thromspondin type I motif"
                                                                                                                                                                         note= "Thromspondin type I motif"
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12-APR-2001; 2001US-00833328
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Scheiflinger P, Antoine G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB, AAD39332
                                                                                                                                                                                                                                                                                                                                                                     40200242441-A2
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ADD94038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MHQRHPWARCPPLCVAGILACGFLLGCMGPSHFQGSCLGALBPGAVSSYLSPGAPLKGRP 60
                aggreenmase, aggreenn; articular extrilage; proteedyten; proteolytic; activities degredation; ontecenthritis; inflammatory foint disease; aggreennitic ontecenthritis; inflammatory foint disease; aggreenmase-associated dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated DNA molecule encoding an aggrecanase polypeptide for producing a purified haman aggrecanase process which can be used to devalop inhibitors of aggrecanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 406; DB 7; Length 1427;
Pred. No. 3.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agostino MJ, Wolfman N, Morris EA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maim 14; SEQ ID NO 8; 24pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.0%;
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                                                                                                                                                                                                                                                                                                                                     25-JAN-2002; 2002US-00057487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Racie LA, Twine NC,
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Best Local Similarity
The 73; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADD94037.
                                                                                                                                                                                                                                US2003105313-A1
                                                                                                                                human, enzyme.
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                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                     05-JUN-2003.
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Human aggrecanase protein

Aggrecanase; osteopathic; antiarthritic; antiinflammatory; human; cartilage; osteoarthritis; inflammatory disease; enzyme.

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This invention relates to the cDNA and protein sequences of a novel human
                                                                                                                            Novel purified aggrecanase polypeptide useful for developing inhibitors and antibodies to the aggrecanase polypeptide. With are useful for zventing aggrecanase-associated condition such as osteoarthritis.
                                                                                                                                                      Claim 11, Page 33-34, 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2004 (first entry)
                                                                                                            NPI: 2002-454602/48
                                                                                                                  N-PSDB: ABK52579.
                                                                                                                                                                                                                                                                                                 Sequence 242 AA;
                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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New isolated DNA molecule encoding an aggrecanase polypeptide for producing a purified human aggrecanase protein which can be used to develop inhibitors of aggrecanase.

Claim 13, SEQ ID NO 1, 24pp; English.

Wolfman N. Morris EA.

Agostino MJ.

Racie LA, Twine NC, WPI: 2003-801251/75

N-PSDB; ADD94032, ADD94033

Twine NC, Aqostino MJ, Wolfman NM, Morris EA,

18-CCT-2000; 2000US-0241469P. 17-CCT-2001; 2001WO-US032458

NO200233093-A2 Homo sabiens. 25-APR-2002. (GEMY) GENETICS INST INC.

Racie LA,

AMHP) AMERICAN HOME PROD CORP. 16-0CT-2001; 2001US-00978979. 25-JAN-2002, 2002US-00057487

US2003105313-A1.

05-JUN-2003

human; enzyme. Homo sapiens. ô

Gaps

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65

3 SCLOALEPOAVSSYLSPGAPLKGRPPSPGFQRQRQRR 41 59 SCLOALEPQAVSSYLSPGAPLKGRPPSPGFQRQRQRRR

AAU79217 standard: protein: 933 AA

15-JUL-2002 (first entry)

AAU79217;

38.2%; Score 204; DB 7; Length 242; 100.0%; Pred. No. 4.56-13; Live 0; Mismatches 0; Indels

Conservative

39;

Local Similarity

Query Match

Sequence 242 AA;

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ch 38.2%; Score 204; DB 5; Length 242; I Similarity 100.0%; Peed. No. 4:6e-13. Jindels 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                         59 SCLOALEPOAVSSYLSPGAPLKGRPPSPGFQRQRQRQRR 97
                                                                                                                                                                                                3 SCLQALEPQAVSSYLSPGAPLKGRPPSPGPQRQRQRQRR 41
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Gaps

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aggrecanase; aggrecan, articular cartilage; proteoglycan; proteolytic; cartilage proteolytic; cartilage proteolytic; antiarthitis; inflammatory joint disease; antiarthitis; castegathitis; antiarthitis; antiarthit
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ADD94031 standard, protein, 242 AA
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                                                                                                                                                                                                                                                                                      Human ADAM-TS-like protein.
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thrombosis, disease;

26-SEP-2001; 2001WO-EP011124. 25-JUL-2001, 2001US-0307393P. 28-SEP-2000; 2000US-0235881P

WO200226999-A2 Homo sapiens. 34-APR-2002.

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ingen purposed contains analysed date of the invention may be used in the diagnosis. Extension and prevention of discretions associated in the discretion is described between the containing the discretion of the containing associated in the discretion of the containing associated in the profilement of discretion of discretion of discretion discretion discretion discretion discretion discretion and discretion discretion and an advantage of the profilement of discretion and a discretion and a discretion of the containing discretion and an assessment of the effects of containing and an assessment of the effects of containing discretion discretion and an assessment of the effects of containing and an assessment of the containing and an assessment of the containing and an assessment of the discretion of profilement of the containing and an assessment of the containing and an assessment of the containing and an assessment of the discretion of profilement of the discretion of the containing and an assessment of the discretion of the containing and an assessment of the discretion of the containing and an assessment of the discretion of the containing and an assessment of the discretion of the containing and an assessment of the discretion of the containing and an assessment of the discretion of the containing and an assessment of the discretion of the containing and an assessment of the discretion of the containing and an assessment of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of the discretion of 
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Elliott VS;
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Lall PG, Walla NK, Hafaila MJA, Gandhi AR, AvYoung J, Bllid
Rankumaz J, Thragavalu X, Lu Y, Warren BA, Lu DAM, Lee BA,
Triboolley CM, Arvinu C, Delegane MA, Yao NG, Khan PA;
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60.5%; Pred. No. 0.21;
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2001US-0260110P.
2001US-0262851F.
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                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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AAC06459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New purified human ADAW-TS-like protein, useful for identifying andulators of protein erotvity for tracting cardiovascular or liver disorder or chronic obstructive pulmonary disease.
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2; Mismatches

23; Conservative

Matches

Local Similarity

Query Match protein

Sequence 933 AA;

Claim 25; Fig 2; 106pp; English

WPI; 2002-383274/41.

Xiao Y;

N-PSDB; ABK49356. (FARB) BAYER AG

ABB98125 standard; protein; 1445 AA

Human PMSM Incyte ID 7473607CD1.

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17-OCT-2002 (first entry)

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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                          The invention cateset or mann applymentations (AXTS) and Three invention cateset or mann applymentations and the encoded process; (AXCONDIT-AADJS10) that eathlist serivity alating or professions or sell differentiation or which may induce production of other options in other cell populations. The professions in other cell populations. The experimentations of the cell populations. The applications are predicted there are action appropriately easier cell series of the cell application of the cell applications are activity, interest or activity, interest or activity, interest or activity, interest or activity, interest or activity in activity, and may be useful in the disposate activity.
                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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monttopic; featuopotenetive, antidabatic; gene therapy; atheroselarosis;
and collectes of classase detection and treatement; camery lables allectare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PTRPKAPSHSAPLLGLALLRMHORHPRAR---CPPLCVAGILACGFLL---GCWGPSHFQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 PRFPREGSPPFPRVFILETROPGPCTKPPFFPPI-----FKLTRPGGRPPKPP 58
NHuman cyptokies, eall proliferation cell differentiation; gene therapy; 
Listana gravitation proliferation cell differentiation; membersonissis; 
Listana gravith factor; manusomodiatory; conter; luukaemia; 
narvous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of cancer loukamenta, nervous system disorders, arthritis and inflammation. Note: The sequence data for this spatent did not form part of the princed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarterioscierotic, anti-HIV, antiallergic, nephrotropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                  Claim 20, SEQ ID NO 20351; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 PORVRACKDPXPQSFRVPGAIPDPPPPDIKGHPPRPGFQXKXKKERK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 QSCLQALEPQAVSSYLSPGA-----PLKGRPPSPGFQRQRQRR 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human molecule for disease detection and treatment MDDT-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.4%; Score 93; DB 4;
27.1%; Pred. No. 0.069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stroke; Parkinson's disease; epilepsy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP98888 standard; protein; 938
                                                                                                                                                                                                                                                            Fang YT, Liu C, Drmanac RT;
                                                                                                                                                            26-PEB-2001; 2001WO-US004927,
                                                                                                                                                                                       28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                                                                              WPI: 2001-514838/56.
                                                                                                                                                                                                                                 HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                             N-PSDB; AAI86390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 115 AA;
                                                                                                   40200164835-A2.
                                                                           Homo sapiens
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                                                                                                                                 07-SEP-2001
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The invention relates to the indication of a number of no-scalise for disease descript and treatment (1907) and gense encoding them. The invention also includes meaning and the scale of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the inv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated peptide molecules for disease detection and treatment, useful for disensing, treating or preventing disorders, e.g. cancer, AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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PPTP-120, autism, aneam, malignam (Ebrough Histoorgoms, vaccine,
PPTPSEALO, nootropic, antianaemic, PRRPEP-120-Agonist, gene herapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YY, Forsythe IJ, Bearling BM, Hafalia AA, Yve H, Xu Y, Forsythe IJ, Bearling BM, Harquia UP, Becha SD, Kable J, Lal FG, Rithardson YM, Lee SY, Lee BM, Tran B, Warren BM, Lu Churudjan R, Sprogne WM, Lal New GJ, Trangayvalu K, Swarmakar A, Gorwad AB, Cafffin DM, Lindquias EM, Elliost VS, Ieon CH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for diagnosing, treating or preventing disorders, e.g. cancer, atherosclerosis, diabetes or stroke.
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24.8%; Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                              2001US-0345384P.
2001US-0343880P.
                                                                                                                                                                                                                                                                                                                                                            12-OCT-2001; 2001US-0328944P
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Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB, ACC44403
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W02003031595-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-2001,
02-NOV-2001;
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                                                                                                               17-APR-2003
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24-SEP-2002; 2002WO-US030474.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Protein Histidine Phosphatase Interacting Partner of 120kD ligand polypebides, useful for diagnosing or treating diseases e.g. autiss, anemia or malignant fibrous histocytomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 GGHKGTGYQAGGLGSPYLRQQAAQAPYIPPLGLDAYPYPSAPLPA--PSPGLK 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 AGILACGFLLGCWGPSHPOOSCLOA--LEPOAVSSYLSPGAPLKGRPPSPGFQ 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human novel contig-encoded polypeptide sequence, SEQ ID NO:3038.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC32956 standard, protein, 539 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kellner R;
                                                                                                                                                                                                                                                                                                                                                                                                                 16-FEB-2001, 2001EP-00103779.
                                                                                                                                                                                                                                                                                                                 25-JAN-2002; 2002WD-EP000753.
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es 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duecker K,
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                                               Homo sabiens.
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resting conditions such as neurodegenerative dissesses, anemias, platelet
dispoteders, wounds, hurns, ulicers, osteoporosa, autofamune diseases or
                                                                                                                                            Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 3038; 1185pp; English.
                                                                                                                                                                                                     Haley-Vicente D, Drmanac RT;
                                                   24-SEP-2001; 2001US-0324631P
                                                                                                                                                                                                                                                    WPI; 2003-371981/35.
                                                                                                                                                      Zhang J,
                                                                                                       HYSE-) HYSEO INC.
                                                                                                                                                                                Ghosh M.
                                                                                                                                                                                                                                                                                   N-PSDB, ADC32189
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15.2%; Score 81; DB 7; Length 539; 32.5%; Pred. No. 6.1;

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34; Indels

7; Mismatches

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Best Local Similarity Matches 40; Conserv

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
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vaccine; peptide therapy; stem cell growth factor; haematopoiesis; itsue growth factor; immunomodistory; cancer; laukaemia, nervous wytem disorders, arrhites; infilammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 15784; 1399pp + Sequence Listing, English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Indels
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25.9%; Pred. No. 2.8;
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Job time : 17:1964 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FBB-2001; 2001WO-US004927
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Best Local Similarity 25.9
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                   W0200164835-A2.
                                                                                                                                                                                                Homo gapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention calcate to valuaging derivatives [1) this attheterial, virtualide protozoacide and inspirate activity. (I) are useful for treatement (of infections interfaction, virtuality protocolo in fungalit, in human accessing a reason of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color of the color o
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                                                                                                                                                                                                                                                                                                                                                                                                                   Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection; medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme.
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                                                                                                                                                                                                                                                                                                                                          Streptomyces viridochromogenes Avi gene cluster polypeptide frame 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.1%; Score 80.5; DB 6; Length 19938;
25.8%; Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weitnauer G, Muchlenweg A, Trefzer A, Bechthold A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid encoding avilamycin synthesis enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 68-301; 319pp; German.
                                                                ABP76680 standard; protein; 19938 Ah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAO01892 standard, protein, 202 AA.
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tes 32, Conserv.
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Matches

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Gaps

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Copyright (0) 1993 - 2604 Compugen Ltd. OM protein - protein search, using aw model: Run on: March 13, 2004, 07,43151, jesuch Lie, 7,67917 Seconds Run on: March 13, 2004, 07,43151, jesuch Lie, 7,67917 Wednesfec	Titie: 10s-10s-25-20PV_1_97 Perfect acces: 534 Perf	nber of DB seq 1 DB seq 1 ressing:	Databae Pablithoph (2012) Pablithoph (2012	Poet No. is the manner of centlar predicted by chance to have a core present than or equal to the some of the result can grained, and is derived by snalygis of the rotal score distribution. Supposition Supposition No. Score Match Length DB 1D Description No.	1 554 100.0 1.0 10.0 10.0 10.0 10.0 10.0 10.	0.141

TITLE OF INVENTION: Anti-Anglogenic Intestinal Peptides, TITLE OF INVENTION: zdint5

YAMAMOTO, GAYLE

APPLICANT

APPLICANT: SHEPPARD, PAUL

PILE REFERENCE: 99-82

CURRENT APPLICATION NUMBER: U3/09/781,090B

CURRENT FILMO DATE: 2002-01-30

NUMBER: OF SEQ ID NOS: 12

SEQ ID NOS: 12

SEQ ID NO 11

LENGTH: 11.20

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APPLICANT: Mery, Gallia
Particont: Walk Harn-down and Proteins and Variants, and Uses Thereof
First Personal Harn-down Uses: Us/Picza, 334
CHEMENT PARTICONTOWNER: US/Picza, 334
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CHEMENT PARTICONTOWNER: US/Picza, 334
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STROMAR: PRESENT: US/Picza, 331
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STROMAR: PRESENT: Version 3.1
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16.0%; Score 406; DB 14; Length 1427;

Bost Local Samilarity 90.6%; Pred. No. 1.18-30;

Matches 73; Conservative 0; Mismacches 1; Indels 0;
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77.54; Score 414; DB 14; Length 1427;
Best Local Similarity 100.09; Pred. No. 1.98-318

Matches 74; Conservative 0; Missarches 0; Indels 0
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Wolfman, Neil
Morris, Elisabeth
TITLE OF INVENTION: Aggrecanase Molecules
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TITLE OF INVESTION Agreedage Volecules
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Twine, Natalie, C.
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Patent No. US20020151702A1
GENERAL INFORMATION:
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US-10-057-487-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , LENGTH: 1427
, TYPE: PRT
, ORGANISM: Homo sapiens
US-10-222-334-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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APPLICANT: Givening-purity, David APPLICANT: Leavy, Gallian APPLICANT: Leavy, Gallian APPLICANT: Leavy, Gallian APPLICANT: Leavy, Gallian APPLICANT: The Leavy Callian APPLICANT: ADMINISTRATION APPLICANT APP

SOFTWARE: Patentin version 3.1

SEQ ID NO 4 LENGTH: 842

US-10-222-334-4 TYPE: PRT Query Match

NUMBER OF SEC ID NOS: 78 ORGANISM: Homo sapiens

Sequence 4, Application US/1022334 Publication No. US20030073116A1 GENERAL INFORMATION:

US-10-222-334-4

Query Match 97.1% Score 492; DB 9; Length 1120; BB 54 Local Similarity 100.0% Fred. No. 44-6-95 MB MRtChas 91; Conservative 9, Mismatches 9; Indels C

, LOCATION (1) (1120) , OTHER INFORMATION: Xaa = Any Amino Acid US-09-781-0808-11

ORGANISM: Homo sapiens NAME/KEY: VARIANT

IYPE: PRT

0; Gaps

Sequence 2, Application US/10222334 Publication No. US20030073116Al GENERAL INFORMATION:

US-10-222-334-2

APPLICANT: Ginsburg, David

77.5%; Score 414; DB 14; Length 842; 100.0%; Pred. No. 1.1e-31; tive 0; Mismatches 0; Indels t

Sest Local Similarity 100. Matches 74, Conservative

Gaps

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NAME: Kapinos Elsan J.
REDISTRATION NUMBER: 12,345
REPRENDE/DOCKET NUMBER: GI 5435p
TELECOMMYNICATION: TRICRATION:
TELECOMMYSTATION: APPLICATION NUMBER: US/60/241,469

FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:

INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 242 amino acids

ADDRESSER. American Home Products Corporation STREET. One Campus Drive CITY: Persippany COUNTRY: USA

CORRESPONDENCE ADDRESS:

NUMBER OF SECUENCES: 6

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APPLICANT: SLREG, Greeney J.
APPLICANT: SLREG, Steven C.
APPLICANT: CHARLES STEVEN C.
APPLICANT: CHARL XLAILENGE STEVEN C.
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OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
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15.7%; Score 84; DB 15; Length 760;
Best Local Similarity 26.6%; Pred. No. 6.9; No. 6.9;
Rether 33; Conservative 11; Mismatches 40; Indels
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LOCATION: (1)...(760)
OTHER INFORMATION: unsure at all Xea locations
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APPLICANT: WILLIAMES AGREE
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THESE OFFICE 194-100 OCC. 514
CURBERT PRICTION OFFICE 194-100 OCC. 514
CURBERT APPLICATION NUMBER: USA/DOS416; RECORPRESS PRICTION OFFICE 194-100
FRICAN APPLICATION NUMBER: DESCRIPTION OFFICE 194-100
FRICANTING NUMBER: DESCRIPTION OFFICE 194-100
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GURRENT PRILING NUMBER: US/10/369,493

GURRENT FILING DATE: US 60/360,039

PRICE RELIGY DATE: 2002-02-28
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; Sequence 12699, Application US/10369493
; Publication No. US203033575A1
; GENERAL IRRORANTION:
APPLICANT: Cap. Yorgwei
APPLICANT: Hinkle, Greeny J.
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Publication No. US20040006026A1
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ORGANISM: Aspergillus nidulans
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SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2002-02-2
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12509
LENGTH: 760
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Query Match 38.2%; Score 204; DB 9; Length 242; Best Local Similarity 100.0%; Pred. No. 5.6=-2. Indels Matches 39; Conservative 0; Mismatches 0; Indels

MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-978-979-1

STRANDEDNESS: unknown

TYPE: amino acid

TOPOLOGY: unknown

APPLICANT Week Agreemase Molecules TITLE OF INVENTION AGREEMEN 109702,077 COURSET PERSENGS 109702,077 COURSET FILING DATE: 2002-01-25

Sequence 1, Application US/10057487 Publication No. US20030105313A1 GENERAL INFORMATION:

US-10-057-487-1

PRIOR APPLICATION NUMBER: 60/241,469

NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin version 3.1 SEQ ID NO 1 PRIOR FILING DATE: 2000-10-18

ORGANISM: Homo sapiens Best Local Similarity Matches 39; Conserva

US-10-057-487-1 Query Match

LENGTH: 242 TYPE: PRT

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38.2%; Score 204; DB 14; Length 242; 100.0%; Pred. No. 5.6e-12; tive 0; Mismatches 0; Indels

S9 SCLOALEPQAVSSYLSPGAPLKGRPPSPGFQRQRQRR 97

39, Conservative

3 SCLOALEPGAVSSYLSPGAPLKGRPPSPGFGRORGRORR 41

US-10-084-846A-6

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1 PGRPTRPKAPSHSAPLLGLALLRMHQRHPRARCPPLCVAGILACGFLLGCWGPSHFQQSC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2h 18, Score 79, DB 15; Length 412, 25 milarity 34.34; Pred. No. 11; 24; Conservative 7; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Applicable; Applicable; Applicable; Pocceine, and Antibodies (Title Open Investigation Notice (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (Applicable) (A
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publication No. US/20030109690A1
GENERAL INFORMATION:
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Publication No. US20040005579A1
GENERAL INFORMATION:
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                                                                                                                                                                           ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                               NAME/KEY: MISC_PEATURE
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                                       TYPE: PRT
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SEQ ID NO 3139
LENGTH: 412
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Best Local 8
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APPLICANT: GROS, PRILITIES
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                                                                                                                                                                                                                                                          Indels 59; Gaps
                                                                                                                      Query Match 15.14, Score 80.5; DB 15; Length 19662; Best Local Similarity 25.84; Pered. No. 4.44.02; Metches 32; Conservative 5; Mismacches 29; Indes 59;
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Publication No. US20040005579A1
GENERAL INFORMATION:
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Publication No. US20030138771A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-09-30
NUMBER OF SEO ID NOS: 552
SOFTWARE: ParentIn Ver. 2.1
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Best Local Similarity 32.6%
Matches 31; Conservative
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LENGTH:

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NAME/KEY: SITE
LOCATION: LOCATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INPORMATION: Xaa
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O'THER INFORMATION: Xaa equals amy of the naturally occurring L-amino acids
13-09-764-877-11s8
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Pred. No. 12;
9; Mismatches 30; Indels 49; Gaps
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
OSPERARE: Patentin Ver. 2.0
SEQ ID NO 1158
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Job time : 8:67917 secs
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Best Local Similarity 27.3%;
Matches 33; Conservative
                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                 PEATURE:
NAME/KEY: SITE
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LOCATION: (98)
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LOCATION: (141
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                                                                                                                                                                                                                                                                                                                 PEATURE:
LOCATION MISC. FEATURE
LOCATION RISC. FEATURE
LOCATION INFORMATION: Xaa equals any of the naturally occurring L-maino acids
OFFICE RIPORPHICAN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE
LOCAFION: (406)
LOCAFION: (406)
LOCAFION: Asa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 PRIPISPLA-SNIGHLIGLRDVRDERQPCHCPGAIPPCPCLPXCRPSSWILSGCPMAISC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PGRPTRPKAPSHSAPLLGLALLR--NHQRH-----PRARCPPLCVAG---ILACGFLLGC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 PLIGLALLRMHORHPRARCPPLCVAGILACGFLLGCWGPSHF0-QSCLQALEPQAVSSYL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 PWCGLKAGRLGLRPP----PPLCS------GQSHLAGPGCLP--RQQVLSS-- 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Gans
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Query Match

14.44, Score 77, DB 14, Length 461,

Bed Local Similarity 32.74, Ped. No. 20,

Matches 32, Conservative 7, Mismatches 43, Indels 1
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14.2%; Score 76; DB 9; Length 216;
Best Local Similarity 35.4%; Pred. No. 11;
Matches 28; Conservative 4; M.Smakiches 25; Indels
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TITLE OF NINGWITCH Mucleic Acids, Proteins, and Antibodies PILL REFERENCE, PCOG.
CURREAT PAPLICATION NUMBER, 105/09/764,877
CURREAT FILLING DATE, 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 GWGPSTGGGDGLFSVE----SHPWVPLVPTLPKPPGTG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 -WGPSHFQQSCLQALEPQAVSSYLSPGAPLKGRPPSPG 87
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; Sequence 1158, Application US/09764877
; Patent No. US20020147140A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 290, Application US/09893737
Patent No. US20020110855A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 SPGAPLKGRPPSPGFQRQR 92
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        PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 4705
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ORGANISM: Homo sapiens
US-09-893-737-290
                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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US-09-893-737-290
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Sequence 4, Appl.
Sequence 4, Appl.
Sequence 4, Appl.
Sequence 4, Appl.
Sequence 7, Appl.
Sequence 7, Appl.
Sequence 7, Appl.
Sequence 1, Appl.
Sequence 10, Appl.
Sequence 10, Appl.
Sequence 10, Appl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GRPTRPKAPSHSAPILIGLALLENHQRHPRARCPPLCVAGILACGF-----LLGCWGP 53
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                                    seguence
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                                                                                                                                                                                                           US-09-252-991A-27853
US-08-738-168B-5
US-09-252-991A-24102
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Patent No. 6551795
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US-09-252-991A-22670
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Sequence 17807, A
Sequence 19289, A
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24340, A
22548, A
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1 PGRPTRPKAPSHSAPLIGLA.....PLKGRPPSPGPQRQRQRR 97
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Sequence 1
Sequence 3
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1. CgpT_6/prodats/2/isas/SA.COMG.ppp.*

3. CgpT_6/prodats/2/isas/SA.COMG.ppp.*

4. CgpT_6/prodats/2/isas/SA.COMG.ppp.*

5. CgpT_6/prodats/2/isas/SA.COMG.ppp.*

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                                                       GenCore version 5.1.6
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US -09-252-991A-29952

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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Maximum DB seq length: 200000000
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Match Length D
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81 80.5 77.5 77.5 77.5 75.5 74.7 74.7

73.5

US-09-252-991A-25176 TYPE: PRT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PGRPT-RPKAPSHSAPLLGLALLR-MAQRHPRARCPPLCVAGILACGFLLGCWGPSH-PQ 57
                                                                                                                                                                                                                                              Query Match 15.2%; Score 81; DB 4; Length 314; 
Best Local Simitarity 30:14; Pred No. 0.42; No. 142; Matches 35; Indets 34; Gaps Matches 35; Indets 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 FLLGCWGPSHPQGSCLQALEPQAVSSYLSPGAPLKGRPPSP---GFQRQRQRQRR 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 RPPRHLYQPAAVPGDLA-GIPLEBARTLRSLPRNGRQPDQYLTHPAAQR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 QSCLQALEPQAVSSYLSPGAPLK-----GRPPS-----PGFQR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
15.1%; Score 80.5; DB 4; Length 324;
Best Local Smilarity 28.7%; Fred, No. 0.5;
Matches 33; Conservative 6; Manaches 33; Conservative 6;
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CURRENT PILING DATE: 1599-02-18 (0.074,788
PRIOR FALING DATE: 1599-02-18 (0.074,788
PRIOR FILING DATE: 1598-02-18
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PRIOR FILING DATE: 1998-02-27
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Patent NO. 6551795
REMERAL INFORMATION APPLICANT: Marc J. Rubenffeld et al.
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Patent No. 6551795
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US-09-252-991A-30702
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SEQ ID NO 24664
LENGTH: 324
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US-09-252-991A-24664
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PARLICANT. MACC. RADMERICAL OR ALL MATCH SEQUENCES RELATING TO SERTCHONOUS.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 PGRPAARRSGRRCCAPYPTHPGVRTGPAPARPAIGCATVAIRPAHPRPRSAVGPHAGTLP 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PGR------PTRP---KAPSHSAPLLGLALLRNGGRHPRARCPPLCVAGILA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 CG-----WPARSHPGHAGGRRGGLRDPWSQG----GEEVVACSSHHRPDAPPPPRPPP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 CGFLLGCW----GPSH-----PQQSCLQALEPQAVSSYLSPGAPLKGRPPSP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 84; DB 4; Length 465;
Pred. No. 0.31;
8; Mismatches 37; Indels 40; Gaps
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CURRENT FILMO DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILMO DATE: 1998-02-18
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30702
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Patent No. 6551795
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Best Local Similarity 28.0%;
Matches 33, Conservative E
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25176
LENGTH: 465
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US-09-252-991A-27050

US-09-252-991A-27050

US-09-252-991A-30702

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 BYRTGCRGOLHPSLVDPLLRACRPAHLSRGOSDRRPLRROPPAPGTRWRRATAHPGDPQR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 PARPEGERNAGREGREPAGREPARRICRRRPRARPRAAAATPAAPPRRHAARAGG- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 GFLLGCWGPSH--FQQSCLQALBPQAVSSYLSPGAPLKGRPPSFGFQRQR-----QR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 PTRPKAPSHSA------PLLGLALLRMHQRHPRA-----RCPPLCVAGILACGF
                                                                                                                                                                                                                                                                                                                                                                           46; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 --STPRPSPRSPGRIGNVPPQP-----APGSPAAGRPSPPGDRSSASRRR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 LLGCWGPSHFQQSCLQALEPQAVSSYLSFGAPLXGRPPSFGFQRQRQRQR 96
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1.Similarity 28:2%; Pred. No. 087; J. Similarity 28:2%; Pred. No. 087; J. Conservative 8; Nismarches 46; Indels 28
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Pred. No. 2.2;
8; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28706, Application US/09252991A
Parent No. 5551795
GENERAL INFORMATION
APPLICANT: Marc J. Rubenfield et al.
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 RPTRPKAPSHSAPLLGLALLRMUORH-
                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23651
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18-09-252-991A-28706
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Best Local Similarity 27.9*
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 31; Conserve
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SEQ ID NO 23651
LENGTH: 273
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 -----GPADRRHRVVHRQRQEPARRQPADDSARRYRRPG--LRGRPGQPGGRELRR 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                     43 ACGFLLGCWGPSHFQQSCL--QALEP-----QAVSSYLSPGAPLKGRPPSPGFQRQRQ 93
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                                                                                                                                         37; Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
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                                                 Ouery Match
14.3%; Score 79.5; DB 4; Length 510;
Seet Local Similarity 28.2%; Pred. No. 1.1;
Seet Local Similarity 28.2%; Pred. No. 1.1;
Seet Local Similarity 37, Indels 4;
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PRIOR FILING DATE: 1998-07-27
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SEQ ID NO 17616
LENGTH: 834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 RORR 97
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US-09-252-991A-17616
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33142

NUMBER OF SEQ ID NOS: SEQ ID NO 19363 LENGTH: 330

Query Match

Matches

TYPE: PRT

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GENERAL PROMATIONS

PARTICANT PROMATIONS

TITLE OF INTERNATIONS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 PARREIPR-PORHPPHRSIRRPAGORRAPRORSAGSAVAA--ACGRAIGIPRRGGPGHGR 124
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13.99; Score 74; DB 4; Length 366;
Metches 33; Conservative 6; Mismatches 33; Indels 36;
Matches 33; Conservative 6; Mismatches 33; Indels 36;
                                                                                                                                                                                                                               ch 13.9%; Score 74; DB 4; Length 271; 15.milarity 31.3%; Pred No. 2.1; 31; Conservative 7; Mismacches 39; Indels 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 14.1%; Score 75.5; DB 4; Length 330; Local Similarity 28.6%; Pred. No. 1.8; All Indels 19; Gaps ees 26; Conservative 12; Mismatches 34; Indels 19; Gaps
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US-09-252-991A-19363
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US-09-252-991A-31668

TYPE: PRT

LENGTH:

US-09-252-991A-31668

US-09-252-991A-17078

RESULT 12

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1 PGRPTRPKAPSHSAPL-----LGLALLRMQRHPRARCPPLCVAGILA--CGFLLGCWG 52
                                                                                  39; Indels 29; Gaps
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13.8%; Score 73.5; DB 4; Length 213;
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Macches 31; Conservative 9; Mismatches 39; Indels 29
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Sequence 1982; Application Us/0935391A
Sequence 1982; Application Us/0935391A
SERVICE CONTROL OF CO 71 -----IRSLAVPGRARRLAGPGMPSRGLRRPRDGGRRRVFRQWRR 110 US-09-252-991A-29952

, ORGANISM: Pseudomonas aeruginosa US-09-252-991A-29952

4 PTRPKAPS--HSAPLIGIALLRAMORHP--RARCPP--LCVAGILACGFLLGCWGPSHFQ 57 Query March 13.7%; Score 73; DB 4; Length 286; Best Local Similarity 32.9% Pred. No. 2.8; Macches 21; Conservative 11; Mismarches 28; Indels 16; Gaps

212 PRRPASPSAGNAAP----ALPRORHRHPLLQRRYPPGRVCSAAVRAAGH-----RQAGQ 261

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Mostadues: 1-660 cabb.
A.Cross-references: BREL:[4/2846; NID:gl125809; PID:gl125810; PIDN:AAA83600.1; CESP:T19f
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A;Gene: CESP:T19D2.1
A;Introne: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 5
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                                          128 CSPTWSCLITEDIGFDLGVTIAHEIGHSFGLEHDGAPGSGC----GP---SGHVMASDGA 180
                                                                                                                 339 CDPARSCAIVEDDGLQSAFTAAHELGHVFNALHDNS--KPCISLNGPLSTSHHVWARVMA 396
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Riletikens (M. R. Suddician Control the coding searchemes of unidentified human genes. X. The complete
A.Reference maker: 21142, MID:9940380; PNID:973681
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A.Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744/1; 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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Abgetusen 2.2155 et
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                                                        A), Sisnusa ; preliminary; translated from GB/BMSL/DDBJ
A), Mosacuda 'type; DNA
A), Rossiduse; 1256 - 4411.
A), Crossis effectnes: BMSL; 863950; PIDN: CAA93287.1; GBP: P2588.3
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32.5%; Pred. No. 1e-17;
tive 27; Mismatches 106; Indels 10;
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A,Nolecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the BMBL Data Library, February 1996
A;Reference number: Z19949
A;Accession: T24896
                                                                                                                                                                                                                                                                                                                                       A, Experimental source: clone F25H8
R, Gajadsty, S.
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es 69; Conserv
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A,Accession: T21371
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Best Local S:
Matches 69
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Length 860; Indels

Query Match 15.3%; Score 174.5; DB 2; Best Local Similarity 24.3%; Pred. No. 9.7e-08; Refectes 54; Conservative 35; Mismatches 87;

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piecery, A.C.; Tiome, B. Lanktor, P. J.; Hall, L.
Arcilla, A. Markillu Digital, 1923, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924, 1924
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C)Superfamily: mouse abtrain abject disinceptin homology
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P.1.52/Dealin: Signal sequence Section predicted <8550.
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                                                           Cispecies: Rattus noivegicus (Norway rat)
Citatus - 17.Apr-1993 #sequence_revision 17.Apr-1993 #text_change 03-Dec-1999
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A./MORlediuge: type: DNA
A./Rosiduae: type: DNA
A./Crosiduae: type: DNA
A./Crosiduae: type: DNA
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C.Species: Incombabditis elegans
C.Dates: 15-Cet-1999 Septons. evvision 15-Cet-1999 Hear_change 18-Teb-2000
C.Datession: 1895s; 724653
S.Podussion: 1
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Indels 25:

98:

Cuery Match
14.8%; Score 168.5; DB 2
Best Local Similarity 26.4%; Pred. No. 6.4e-07;
Best Local Similarity 26.4%; Nr. 6.4e-07;
Alsmatches 98

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RESULT 7 S28259

A.Reference number: 219917
A.Accesson: T24653
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA

A.Experimental source: clone T07C5 C:Genetics:

A, Residues: 1-1444 <WI2> A.Gene: CESP: C02B4.1

submitted to the EMBL Data Library, July 1995

9,Experimental source: clone C02B4 R,McMurray, A.

submitted to the EMBL Data Library, July 1995

A.Reference number: Z19031 A.Accession: T18856

DB 2; Length 1444;

165 GSGCGPSGH-VMASDGAAPRAGLAMSPCSRRQLLSLLSAGRARCVWDPPRP 214

Experimental source: clone F5787

A, Accession: T22836

A:Gene: CESP:F57B7.4

Local Sim.

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Query Match

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Soft Concentrate (Fig. 14.24.-) N-1 precureor - carpet viper (Concentration identification along) for concentration identification along for concentration (State of concentration along for concentration along for concentration (State of concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentration along for concentra
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R.PACER, F. BOMATE, T. Talkia, D.D. H. DOSHOON, A.F. Stringer, B.; Grahim, R.; Russel.
R. A.Tiles & Res. Oceann. 230, 335-339. 1599 11Acc attacher, B.; Grahim, R.; Russel.
A.Tiles Dycession of emisses of a somewine of a somewine of a somewine of a somewine or a somewine of a somewine of a somewine of a somewine of a somewine of a somewine of a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a somewine or a som
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C.Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 31-Dec-2000
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R;Hexren, B.; Raines, E.W.; Ross, R.
submitted to the EMBL Data Library, January 1996
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7,146/Active site: Glu #status predicted

A, Experimental source: venom A;Molecule type: protein A;Residues: 1-429 <TAK>

A;Status: preliminary

25.0%; Conservative

Local Similarity

53, Query Match

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113 LNSMCHPRNSVGLIQDHSPINLLMGVTMAHELGHNLCMEHD---GKDCLRGASLCIM-RP 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.9%; Score 135.5; DB 2; Length 814;
12.0%; Pred, No. 0.00032;
Conservative 22; Mismatches 62; Indels 31,
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F:143/Active site: Glu #status predicted
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C;Genetics:
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C; Superfamily: unassigned disintegrins; disintegrin homology
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A;Molecule type: mRNA
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Best Local Similarity
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Gaps 10.9%; Score 124; DB 1; Length 202; 23.4%; Pred. No. 0.00066; zive 38; Mismatches 100; Indels 26; Conservative Local Similarity es 50; Conserv

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179 GAAPRAGLAMSPCSRRQLLSLLSAGRARCVMDPP 212

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score greater than or equal to the score of the result being printed,
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Copyright (c) 1993 - 2004 Compugen Ltd.
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WEDLINE-21264577, PubMed=11278086;
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Cal S. Arguelles J.M., Peranades P.L., Lopes-Otin C.;
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Nammalia, Estilesta, Primates, Catarthini, Hominidae, Homo.
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38.4%; Pred. No. 3.7e-23;
1ve 35; Mismatches 97; Indels
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ADAMTS-7.
METALLOPROTEASE.
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11. Symptomical-Marines in long indocement;

20. defended in Administration in Marines in Administration in Administration in Administration in Administration in Administration in Computer (WPP 107007);

11. Description in Classification in Computer (WPP 107007);

11. Description in Classification in Classi
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Butheris, Rodentis, Sciurognathi, Muridae, Murines, Mus
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PRT: 1224 AA. AT16 HUMAN STANDARD; QBTE\$7; QBIVE2; 10-OCT-2003 (Rel. 42, Created) RESULT 5 AT16 HUMAN ID AT16 HU AC Q8TE57; DT 10-OCT-

10-0077-2003 (Rel. 42, Last sequence update) 15-WAR-2004 (Rel. 42, Last manneation update) ADMNFS-16 precursor (RC 3-4.72--) (A districgrin and metalloproteinase with thromospondin mette 16) (ADMN-TS 16) (ADMN-TS16). "Cloning, expression analysis, and structural characterization of seven novel human ADAMTSA, a family of metalloproteinases with distincents and thrombospondin-1 domains."; Homo sapinam (Human) Shibanah Shibanah Shibanah Marabilar Buteleostomi; Shkaryota: Wetacas, Chordara, Craniara; Vettebrata: Buteleostomi; Memmaliar, Butiserias, Primares; Catarthini; Hominidae; Homo. NCBLTaxina506; MEDLINE-21856482; PubMedall867212; Cobs S. Obaya A.J. Llamazares M., Garabaya C., Quesada V., SEQUENCE OF 204-1224 FROM N.A. (ISOFORM 1) (ISOFORM 2) Gene 283:49-62(2002) SECUENCE FROM N.A. TISSUE=Brain,

Nagan C. T. Kilono B. Orbana O. T. Orbana O. -1- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;

[soId=Q8TE57-1; Sequence=Displayed; Name=2;

Taoid-08T87-2, Sequence=1SP 007664, VSP 007665, and kidney and in adult professe and overy.

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-!- PTM: The precursor is cleaved by a furin endopeptidase (By similarity). -i- SIMILARITY: Belongs to peptidase family M128.
-i- SIMILARITY: Contains idsintegrin-like domain.
-i- SIMILARITY: Contains 6 TSP type-1 domains.
-i- SIMILARITY: Contains 1 FLAC domain.

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EMBL, AJ315734, CAC66015.1; -... EMBL, AB09599; BAC23125.1; -... MEMCDS, MI2.026; -... Genew; HCNC:7108; ADAMTS16. MIM, 607510;

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

GCBI TaxID=9606,

SÉQUENCE FROM N.A. Casas C., Pittchard N.A., Estivill X., Arbones M.L.; "Cloning, characterization and mapping on human circmosome 21 orthologue of murine Adamts-1.", Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases SEQUENCE FROM N.A., AND FUNCTION.

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Vazquez F., Hastings G., Orrega M.-A., Lane T.F., Olkemus S., Contacto M., Irrola-Ariepp W.I. A., Manan. cetcholog of ADMYRS-1, and WERFL a members of a new family of processes with anglo-inhibitory activity."; mily of proteins with anglo-inhibitory activity.": Biol. Chem. 274:23349-23357(1999). MEDLINE=99367466; PubMed=10438512;

MEDITAGO204118; PAMES-1078620; Kinzmann B., Weiss B., Oldsack J., Schmitt A.O., Platraky C., Kinzmann B., Weiss B., Oldsack J., Schmitt A.O., Platraky C., Platra SEQUENCE FROM N.A. TISSUE-Endothelial cells,

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MEDINE-20181126, Pubwed-10718138, Nagase A., Zhikaswa M., Ohara O., Nagase A., Kiknon K., Ishikawa K.-I., Hikaswa K.-I., Huraswa K.-I., Ishikawa Penses XVI Prediction of the coding sequences of unidentified human genes. XVI the complete sequences of 150 new CDNA clones from brain which code TISSUE-Brain:

SEQUENCE FROM N.A. MEDLINE=20289799; PubMed=10830953; for large proteins in vitro."; DNA Res. 7:65-73(2000).

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Nature 405:311-319(2000).

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319 PEVTSNAALTIRNPCNWOKQHNPPSDRDAEHYDTAILFTRODL---CGSQTCDTLGWADV 375 PNITANLISSLESVCGWSQTINPEDDIDFGHADLVLYITRFDLELFDGRR--QVRGVIQL 124 72-755-2001 (sel. 41, Created)
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Bukaryota Metazoa Chordata; Crantata, Vertebrata, Buteleostomi; Mammalia Euthoria; Primates; Cararnini; Hominidae; Homo. 17. Taxio-9606; SEQUENCE FROM N.A.

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This actions form entry in copyright. It is produced through a collaboration between the Sarias institute of Bioinformatics and the Figure outeration. The European informational institute of these are no restrictions on its way. To comprose a neutrinoction on the many of the company of the - SIMILARITY: Belongs to peptidate family MIDB.
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- SIMILARITY: Contains 5 TSP type-1 domains.

EMBL: AF163762; AAG35563.1; -.

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214 YVETLVVADROMVAYHGRRDVEQYVLAIMMIVÄKLFQDSSLGSTVNILVTRLILLTEDQP 273
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-- DOMAIN The spacer domain and the TSP type.1 domains are important for a tight interaction with the actracellular mail type.
-- Type: preuneor is cleaved by a furin andopeptialse (SY MY) The preuneor is cleaved by a furin andopeptialse.
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                                                                                                                                                                                                                                                                                                                lydrolase, Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matrix (By similarity).
-:- INDUCTION: Down-regulated in endothelial cells derived from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
-!- SIMILARITY Belongs to peptidase family ML2B.
-!- SIMILARITY: Contains 1 disintegrin-like domain.
-!- SIMILARITY: Contains 3 TSP type-1 domains.
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BY SIMILARITY.
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TSP TYPE-1 3.
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EMBL, AF304446; AAG29823.1; -.
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REGOTTE, REGOLZÍO INTÉRTÉREZH. 2; FALSE, NEG.
REGOTTE, REGOLZÍ ZANC REGORSER, I.S.
PORTOLES REGALLEGUESSER, ZANC REGORZÍO SEGNAL (OLYOQUETCEIN; Dymogen;
PORTOLES KRAILOGUESSER; ZANC REGORZÍO SEGNAL (OLYOQUETCEIN; Dymogen;
PORTOLES KRAINGEILLIA: METALY, MERZHI, D'ALBANG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYSTEINE SWITCH (POTENTIAL).
ZINC (CATALYTIC) (BY SIMILARITY).
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DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PSE0215; ADAM MEDRO; 1.
PROSITE, PS00427; DISINIBGRIN 1; FALSE NEG.
PROSITE, PSS0214; DISINIBGRIN 2; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSP TYPE-1 2.
TSP TYPE-1 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                         Interpro: IPRO.05866 ADM. Cysteine.
Interpro: IPRO.0506 ADM. Cysteine.
Interpro: IPRO.0507 Pept M. Zh. B6.
Interpro: IPRO.0509; Peptidae. Miza.
Interpro: IPRO.2807; Peptidae. Miza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADAMTS-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPACER.
TSP TYPE
              Interero, IRRODOMS4, TSP1.

Interero, IRRODOMS4, TSP1.

Interero, IRRODOMS5, TSP1.

Figur, PRO1421, Reprolysin.

Figur, PRO1421, Reprolysin.

FRINTS, PRO1405, TSP2.

SWART, SWOOSS, TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48
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968 A.R.;
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ACT SITE
METAL
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7 HIBILVAVGPDVPQAHQEDTERYVLTNINIGABLIRDPSLGAQFRVHLVKAVILTEPEGA 66 h 26.1%; Score 297.5; DB 1; Length 968; [Similarity 29.6%; Pred, No. 9.78-18; Conservative 36; Wismatches 101; Indels 15; Gaps 64; Conservative 36; Wismatches 101; Indels 15; Gaps Query Match Local Matches

260 YVETMLVADQSMADFHGSGLKHYLLTLFSVAARFYKHPSIRNSISLVVVKILVIYEEQKG 319 6.7 PNITANLISSLISVCGWSQTINPEDDIDPGHADLVLYITRFDLELPDGNRQVRGVTQLGG 126 20 PEVTSNAALTLANFCHWOKOHNSPSDRDPEHYDTAILPTRODL-CGSHTCDTLGMADVGT 378 27 ACSPIWSCLITEDIGFDLGVITAHEIGHSFGLEHDGAPG----SGCGPSGHVMAS----

> 9 Š 9 ò g ò

379 VCDPSRSCSVIEDDGLOAAFTTAHELGHVFNNPHDDAKHCASLNGVTGDSHLMASMLSSL 438 .78 DGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPR 213 139 DHSOP----WSPCSAYMVTSFLDNGHGECLMDKPO 469

metalloproteinase Homo spylens (Human). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Butheria, Primates; Catarihini, Hominidae, Homo. 7755 TANDRAM STANDAD, PRT, 1935 AA.
1007256; CRRACAD, CREEGA,
11-077-2001 (Red. 42, Leme and equence update)
11-077-2003 (Red. 42, Leme and equence update)
11-077-2003 (Red. 44, Leme and equence update)
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11-077-2003 (Red. 44, Leme and equence update)
11-077-200

ECCCOSSEERING

Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A., Maki R.A.; was novel member of the ADAM-TS/Wetallospondin gene IISSUE=Fetal; MEDLINE=20396138; PubMed=10936055; SEQUENCE FROM N.A. (ISOFORM 3). NCBI TaxID=9606;

family."; Genomics 67:343-350(2000).

MEDICARES RENAL AL (RECORDA IL) AND FINATION.
MEDICARES AND MASSIANT AND MASSIANT AND INDEED AND IN THE STATE AND INDEED AND IN THE STATE AND INDEED AND IN THE STATE AND INDEED AND IN THE STATE AND IN THE STATE AND INTERPRETATION AND INTERPR SEQUENCE OF 159-1935 FROM N.A. (ISOFORM 2).

WEDLINGSCHILLS, PARAGOTORISS, VILLERSAN N. CORRE D. 1970-1970 STREET, XANDO R. Inhikana N.-1., Hircesana N. Obare D. 1970-1970 C. Inhikana N.-1., Hircesana N. Obare D. 1970-1970 C. Obare December On Man. The Conference of Manhatter Daniel D rissum=Brain;

-- CATALTIC ACTIVITY: Cleaves aggreean at the 1838-Glu-|-Ala-1839 established and versions at the 1845-Glu-|-Ala-1459 glu-|-CORACTOR: Stands I stand on per submit (By smalatity).
-- CORACTOR: Stands I stand on per submit (By smalatity).
-- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular. and versican.

Name=2; Synonyme=Long: Igoli4e9P2N4-1. Sequence=VSP 007548, VSP 007549; Note=May result from the retention of an intron in the cDNA Lasting to a prematurate etop codon; =:- ALTERNATIVE PRODUCTS: EVENT-Alternative splicing, Named isoforms=3; Name=1, Synonyms=AbhNTS-9B; Isoid=G9P2N4-3; Sequence=Displayed; matrix (By similarity).

TRANSIS, SELECTION OF SELECTION

-i- PIM: The precursor is cleaved by a furin endopeptidase (By

similarik).

- SIMILARITY: Balongs to peptidase family MIZB.
-- SIMILARITY: Contains 1 disintegrin-like domain.
-- SIMILARITY: Contains 10 M domain.
-- SIMILARITY: Contains 15 TSP type-1 domains.

Sp. Carlo	Oppidane activity; TAB. Inserin. Insert	DOGASI 68 6 67 15 15 15 15 15 15 15 15 15 15 15 15 15
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or send an er	ail to	licens	. (3
SMBL; AF26191 SMBL; AF48880	3; AM	789106.1	
SMBL; AB03773 4SSP; P15167;	JATE	192550.1	
Senew; HGNC:1	3202;	ADAMTS9	٠
30, GO: 000823	77	netallop	eptidase activity, TAS.
30, 90:000651	9	Jycopro	ntein catabolism; TAS.
InterPro; IPR	00136	2; Disin	tegrin. MioA Mi2B.
InterPro; 1PR	00129); Pept	M_zn_BS. dase_M12B.
InterPro; IPR InterPro; IPR	000287), Pepti	dase_M12B_N.
Pfam, PF01562	Peo	M12B pr	opep; 1.
Pfam, PF0090	t ap	1, 11.	1.
SMART; SMUUZU	9; TSI	P1; 12.	
PROSITE; PSOO	546,	YSTEINE	SWITCH, FALSE NEG.
PROSITE, PS00 PROSITE: PS50	214:1	DISINTEG	RIN 1; PALSE NEG.
PROSITE, PSSO	092;	FSP1, 14	
PROSITE, PSOO Tydrolase; Me	tallor	ZINC PRO	al;
Repeat; Extra	cellul	lar matr	ive splicing.
PROPER	161	287	POIDMILAD.
CHAIN	88	1935	į
DOMAIN	m 60	587	55
DOMAIN	88	643	1 1
OMAIN 6	44	752	CYS-RICH.
NI WOO	19	936	H
DOMAIN	93	1997	TSP TYPE-1 3.
DOMAIN 10	25	100	1 -
DOMAIN 11	200	1166	-1 -
DOMAIN 12	41	1296	- 8
DOMAIN 13	28	1379	6.
DOMAIN 13	262	494	- -
DOMAIN 14	16	1555	1
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DOMAIN 17	35	1935	
DOMAIN	98	96	SWITTCH (DOWE
GTAL 4	34	434	PALYTIC)
ACT SITE 4	9 8	435	RITY.
GTAL 4	4.4	444	ZINC (CATALYTIC) (BY SIMILARITY).
CARBOHYD	12	112	N-LINKED (GLCNAC) (POTENTIAL).
ARBOHYD 2	32	271	(GLCNAC) (POTENTIAL)
CARBOHYD	0.0	749	(GLCNAC)
ARBOHYD 12	3 6	840	(GLCNAC) (POTENTIAL) (GLCNAC) (POTENTIAL)

TISSEMLATION, Pubmedioussis; C. Ortega N.A., Lans T.P., Oldemus S., Vargette, C. Ortega N.A., Lans T.P., Oldemus S., Vargette, S. Ortega N.A., Lans T.P., Oldemus S., Vargette, S. A., Albana Cathologo G. Zaharsi, and METFL. are embers of a new femily of process with magic -nabilitatory activity.'; J., Bol., Chem. 274:22349-22357(1999).

SEQUENCE FROM N.A. NCBI TaxID=9606;

SEGENCE Or 1854-44 PROOF N.A.

SELLEME COTSIST, DAMAGINGOUS N. F., Apre S.S.; IT JOCATED ON CONTRIBUTION OF SELLY APPROACH SEL

	ś	P 354	G 125	A 180		
	Gaps	EPEGA INEQDG	GVTQI	MASDO 		
POTENTIAL). (in 1soform (in 1soform cform 2).	16;	LELLVANGPDVPQAHQEDTERYVLTAINIGAELLRDPSLGAGFRYHLYGYVLLTEPEGAP 	NITANLISSILSVCANSQTINPEDDTDPQHADLVLYITRPDLELPDGNRQVRGVTQLG - - - - - - - - - - - - -	GACSPTASCLIZEDTGFDLGVTIAHBIGHSFQLBHDGAPGSGCGPSGHVMASDGA TICDYSCSCSISEDGGSGLSTAFTAHBIGHVFNMHDDNNKCKEGVKSPQVMAPTLN		
(porential description of the control of the contro	Length 1935; Indels 1	RVHLV.	LELPD : ICRAH	GPSG- KREGV		
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	DB 1; I 6.4e-17; hes 95;	LRDPS	ADLVLY HTAVI	CEHDGA CPHD-		
SP 00 CIL	292;] No. 6.	NIGAEI 	H-62	GHVFNI	VWDPP ::-	
	Score 292; Di Pred. No. 6.4 38; Mismatches	VLTNL	RDDTD	TAHELG	GYGEC	
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1986 1806 1072 1935 1629 46 96 1182 96 3117 1337	25.6%; 31.0%;	POAHOF	SVCGWS	TEDTOS 	SRRQLI ::: SRKYIT	
3	ilarity 31.0 Conservative	VGPDVI ADMRM	TSSLL TTLK	SCLIT	AWSEC	
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63; Conservative 36; Mismatches 104; Indels
   Matches
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2).
   TISSUE SPECIFICITY: Higly expressed in adult and fetal lung, lower expression in brain, placenta, heart, stomach and fetal brain and
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
B - S (IN REF. 2).
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                                                    -i- DOWAIN: The spacer domain and the TSP type-1 domains are in
for a tight interaction with the extracellular matrix.
-- PTM: The precursor is cleaved by a furth endopeptidate (by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S7D70EE03D5739D3 CRC64;
                                                                                                                -i- SIMILARITY: Belongs to peptidase family M128.
-i- SIMILARITY: Contains 1 dishinegrin-like domain.
-i- SIMILARITY: Contains 2 75P type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-PRO.
ZINC (CATALYTIC)
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DISINTEGRIN-LIKE.
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ZINC (CATALYTIC)
ZINC (CATALYTIC)
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CYS-RICH.
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                                                                                                                                                                                                                                                                                                                EMBL, AF060153, AAD48081.1, ..
                                                                                                                                                                                                                                                                                                                             EMBL, AF175283; AAF25806.1; -. HSSP; P34179; 11AG. MEROPS; M12.26; ADAMTS8. Genew: HGNC:224; ADAMTS8.
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METĀL
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Score 285, DB 1, Length 890; Pred. No. 1e-16;

25.0%;

Query Match Best Local Similarity

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281
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EMBL, AP14813; AAD41494.1; ...
EMBL, AY044847; AAL02262.1; ...
PTR, TO0355; T00355.
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TSP TYPE-1 4.
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856 NIEVLIGVDDSVVOPHGKEHVOKYLLTLANIVNEIYHDESLGAHINVVIVRIILLSHAKS 327 66 APNI-TANLISSLLSVCGWSQ-TINPEDDIDPGHADLVLYITRFDLELFDGNRQVRGVTQ 123 328 MSLIEIGNPSOSLENVCRMAYLOOKPDIDHDEYH-DHAIFLIRQDF----GPSGMGGYAP 382 7 HIBLLVAVGPDVFQAH-QEDTERYVLTNINIGAELLRDPSLGAQFRVHLVXXVILTEPEG 65 37; Mismatches 89; Indels 14; Gaps 24.1%; Score 275; DB 1; Length 1213; 34.0%; Pred. No. 1.1e-15; 72; Conservative Local Similarity Query Match Best Loca Matches

g ò 용 124 LOGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPGSGCGPS---GHVWASDGA 180

	8 9 8 8 8 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4	131 VTOMCHPRESTLANDSDESAFVANHERDFORGERANDSDEFFLORENDSTRAGENDARD (41) 442 AATREMERSCEQUESAFVANHERDFORGERANDSDEFFLORENDSTRAGENDARD (41) 442 AATREMERSCEQUESAFVANHERDFORGERANDSDEFFLORENDSTRAGENDSDEFFLOR	PROSITE; PSSOUND; TEAL; 1. PROSITE; PSSOUND; TEAL; 2. PROSITE; PSSOUND; ZINC_PROTEASE; 1.
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LINKED GLCKAG. POTBWTALI.
N-LINKED GLCKAG. POTBWTALI.
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ARG-RICH.

ZINC (CATALLTIC) (BY SIMILARITY).

BY SIMILARITY.

ZINC (CATALLTIC) (BY SIMILARITY).

ZINC (CATALLTIC) (BY SIMILARITY).

ZINC (CATALLTIC) (BY SIMILARITY).
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     POTENTIAL.
BY SIMILARITY.
ADANTS-IT.
METALLOPROTEASE.
DISINTSCRIN-LIKE.
TSP TYPE-1 1.
                                                                                                 SPACER.
TSP TYPE-1 2.
TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 5.
PLAC.
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1095 AA;
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Query Match Senilarity 24.0%; Score 274; EB 1; Length 1095; Base Local Schalarity 11.2%; Fred No. 1.1.1.9; Indels 19; Gaps 6; Matches 69; Conservative 5, Mismitches 99; Indels 19; Gaps 6;

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413 MSGEWVKGRNPSDLSWSSCSRDDLENFLKSKVSTCLLVTDP 453

Search completed: March 13, 2004, 07:39:53 Job time : 4.45833 secs

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5.1.6	Compugen
version	- 2004 Cc
enCore	1993
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- procein search, using sw model	March 13, 2004, 07:30:14 ; Search time 21.1771 Seconds (without alignments)
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OM protein	Run on:

3188.394 Million cell updates/sec 1141 1 AAGGILHLELLVAVGPDVFQ.....QLLSLLSAGRARCVWDPPRP 214 US-09-836-712-2_COPY_98_311 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Scoring table:

1017041 Total number of hits satisfying chosen parameters: 1017041 segs, 315518202 residues Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database

Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

SUMMARIES

Description	2	Osbkyl mus musculu	Callb3 mus musculu	Q8mrls drosophila	O9w493 drosophila	OBCG28 mus musculu	Q8ne26 homo sapien	Q8hzm8 equus cabal	Q8k206 mus musculu	Q19791 caenorhabdi	Q7ys95 bos taurus	Q8k384 mus musculu	Osbnj2 mus musculu	Qabkal mus musculu	Q9wlz6 drosophila	Ospzdl mus muscalu
QI.	096137	OSBKY1	081183	CHMRLS	Q9W493	080028	QBNE26	OBHZMB	08K206	019791	Q7Y895	Q8K384	Q8BNJ2	OBBKA1	9ZTM60	Q8BZD1
80	-	ri	Ħ	s	S	7	4	9	=	'n	w	:	Ħ	7	s	Ξ
Length DB	1427	1009	1600	769	1059	1070	967	759	900	2165	839	833	845	1092	1001	497
% Query Match	100.0	30.4	30.4	29.8	29.8	27.0	26.7	26.6	26.2	25.9	25.5	25.1	25.1	24.8	23.1	22.9
Score	1141	347	347	340	340	307.5	304.5	303.5	298.5	295	291	286	286	283.5	263.5	261.5
Result No.	-	64	m	4	S	9	1	00	o.	70	11	12	13	14	15	16

Q8t458 drosophile	Osmmel drosophile	Q8bgp4 mus musci	Q8sxb0 drosophil	Q22580 caenorhab		Q95n24 equus cab	O91vs9 mus musc	Osch80 cavia po	snu	Q8c7z0 mus musc	Q9g154 oryctolag	aenorha	OBiu50 caenorhab	aen	108 omou 64x980	agk		o xenopu	Q90499 echis py	des omou	GBn0w6 home sapi-	86p79	ರ	20 agkistr	dros	_	3awis	Q7t1t3 bothrops	
087458	OBMEI	· QBBGP4	QBSXBO	022580	QBMYAB	095N24	Q91VS9	QBCHB0	QBCAB2	Q8C7Z0	09GL54	Q7Z291	CBINSO	019204	Q86XK9	Q9PVR9	020930	012960	090499	Q8NEK2	OBNOWE	66079	OHAA60	090220	Q8MT72	QBCDV3	OBAMIS	Q7TIT3	
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22.2	22.2	19.7	18.6	'n	14.8		14.3		14.0	-		13.5		13.5		-			11.9			11.4		11.3			11.1	11.0	
253.5	253.5	224.5	212	6	168.5	w	163	162	160	160	159	153.5	153.5	153.5	150	146	146	139	135.5	134	133.5		130			128	127	126	
17	00	13	50	21	22	23	24	25	56	27	28	53	30	31	33	33	34	35	36	3.7	38	39	40	41	54	43	44	45	

ALIGNMENTS

67 PNITANLISSLLSVÇGWSQTINPEDDIDPGHADLVLYITRFDLELPDGNR--QVRGVTQL 124

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SANDANCATANA (TITSORTHANDALISAGES),
MENDINGATANA (TITSORTHANDALISAGES),
MENDINGATANA (MANAGALISAGES),
MENDINGATANA (MANAGATANA (MANAGATANA (MANAGATANA MANAGATANA (MANAGATANA MANAGATANA                                                                                                                                                                                                                                                                              75 AAGGILHLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVRAVIL 134
                                                                                                                                                                                                                                                                                                                                          61 TEPEGAPNITANLISSLLSVCGWSQTINPEDDTDPGHADLVLYITRPDLELPDGNRQVRG 120
                                                                                                                                                                                                                                                                                                                                                                                                    13S TEPEGAPNITANLISSILSVCOMSQTINPEDDIDPGHADLVLYITRFDLELPDGNRQVRG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAFGSGCGFSGHVMASDGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 VTQLGGACSFTWSCLITEDIGFDLGVTIAHEIGHSFGLEHDGAPGSGCGPSGHVMASDGA 284
                                                                                                                                                                                                                     9
                                                                                                                                                                                                                     1 AAGGILMLELLVAVGPDVPQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKAVIL
75 1427 VON WILLBBRAND FACTOR-CLEAVING PROTEASE
1427 AA; 193632 MW; BBIBC3AABC1A4442 CRC64;
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa; Chordata; Cranista; Vertebrata; Buteleostomi,
Mamalia Butleria, Rodentia; Sclurognathi; Muridae; Musinae; Ms.
NCBI Taxib=10990;
                                                                             Query Match 100.0%; Score 1141; DB 4; Length 1427; Seef Local Similarity 100.0%; Pred. No. 1.8e-39. Indele 0: Marmatches 24; Conservative 0; Mismatches 0; Indele 0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113352 NW: 7863218CFFE0FDB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
ADANTS-12 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 APRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 APRAGLAWSPCSRROLLSLLSAGRARCVWDPPRP 288
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      CHAIN
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8 LELLVAVGPDVFQAH-QEDTERYVLTNLNIGAELLRDPSLGAGFRVHLVKAVILTEPEGA 66

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Gabs

8

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312 LKIVHHAEKTLSSFCKMQKSINPKSDLNPVHHDVAVLITRKDI-CAGVNRPCETLGLSQL 370
                                                                                 125 GGACSPIWSCLITEDIGFDLGVTLAHEIGHSPGLEHDGAPGSGCGPSG---HVWASDGAA 181
                                                                                                                                          371 SGMCQPHRSCNINEDSGLPLAPTLAHELGHSPGIQHDGKE-NDCEPVGRHPYIMSQQIQY 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 VETLIVVALTKIVERHIGSENVESYILLIMARVIGLFHSPSIGNLVHIVVVRLILLEBEEQG 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 LKIVHHAEKTLSSPCKWQKSINPKSDLNPVHHDVAVLITRKDI-CAGVNRPCETLGLSQL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12S GGACSPIWSCLITEDIGVILAHEIGHSPGLEHDGAPGSGCGPSG---HVMASDGAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 SGMCQPHRSCNINEDSGLPLAFITAHBLGHSFGIQHDGKB.NDCBPVGRHPYIMSQQIQY 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Last annotation update)
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                                                                                                                                                                                                                                                                        430 DPTPLTWSKCSKBYITRFLDRGRGPCLDDIP 460
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Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
                                                                                                                                                                                                                                  Donophila melanogaster (Fruit fly).
Blastroca Meazas thribropda i Seasoda Inserta, Ptarygota;
Robers, Endopropydes Depesa Resolyces; Muscomorpha;
Robers, Endopropydes Depesa Resolyces; Muscomorpha;
Robers, Companies of Prospilla.
01-MAY-2000 (TERMBLrel. 12, Created)
01-077-2000 (TERMBLrel. 22, Last sequence update)
01-077-2003 (TERMBLrel. 25, Last amnotation update)
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Bankaryosa, Wetasoa Arthropoda, Bakapoda, Insecta, Pterygota,
Meoptera, Endopterygota, Dipera, Brachycera, Musconorpha)
Ephdroiden, Droeophilidae, Drosophila.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 25, Last annotation update)
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206 YVETLVVADDOMVAYHGRRDVEQIVLAIMNIVAKLEQDESLGAIVNILVTRLILLIEDQP 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 TLEITHHAGKSLDSFCKWQKSIVSHSGHGNAIPENGVANHDTRVLITRYDICIYKKFCG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 HLELLYANGPDVFQAH-QEDTERYYLTNLMIGAELLRDPSLGAGFRVHLVKAVILTEPEG
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The structure of Angarday R. A. Massaya, R. A. Massaya, R. A. Massaya, R. A. Massaya, R. A. Massaya, R. A. Massaya, R. A. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Massaya, R. Mass
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 ---VMASDGAAPRAGLAWSPCSRRQLLSLLSLLSAGRARCVWD-PPR 213
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182 PRAGLAWSPCSERQLLSLLSAGRARCYWDDRRP 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 PEVTSNAALTLANFCNWQKQHNPPSDRDABHYDTAILFTRQDL---CGSQTCDTLGMADV 375
                                                                                                                                                                                                                                                                                                                                       99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 GGACSPTWSCLITEDIGFDLGVTIAHEIGHSFGLEHDGAPG----SGCGPSGHVWAS--- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376 GTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAXQCASLNGVNQDSHAMASMLS 435
                                                                                                                                                                                                                                                                                                                                       7 HLELLVANGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKKVILTEPEGA
                                                                                                                                                                                                                                                      Owery Watch 26.7%; Score 304.5; DB 4; Length 967; BB 858 Local Similarity 29.8%; Pred. No. 8.3e.19, Zides 19; Gaps Matches 55; Conservative 40; Materaches 94; Indels 19; Gaps
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Referencia, Peteacoa, Chordate, Craniata, Vertebrata, Euteleogtomi;
Mammalis, Eutheria; Perissodactyla, Equidae, Equus.
VCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.6%; Score 303.5; DB 6; Length 759;
83410 MW; C18E4C048918C8E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 -- DGAAPRAGLAWSPCSRROLLSLISAGRARCVWDPPR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 NLDHSQP----WSPCSAYMITSFLDNGHGECLMDKPQ 468
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SEQUENCE
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51 YVETMLVADOSMARFHGSGLKHYLLILFSVAARLYXHPSIRNSVSLVVVKILVIYEEQKG 110
                                                                                                                                                                                                                                                                                                                                                                            67 PNITANLISSLLSVCGWSQTINPEDDIDPGHADLVLYITRFDL---ELPDGNRQVRGVTQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 PEVISNAALTLANFCNWQKQHNPPSDRDAEHYDTAILFIRQDLCGAQTCD----TLGMAD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 LGGACSPTWSCLITEDTGFDLGVTIAHBIGHSFGLEHDGAPG----SGCGPSGHVWAS-- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 VGTICDPSRSCSVIEDDGLQAAFTTAHELGHVFWMPHDDAKQCASINGVNRDSHMWASML 226
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                                                                                                                                                          7 HIELLVAVGPDVFQAHQEDTERYVLTNINIGAELLRDPSLGAQPRVHLVKWVILTEPEGA 66
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | Page | 
Best Local Similarity 30.1%; Fred. No. 7.5e-19;
Matches 66; Conservative 38; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausherg R., Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 --- DGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPR 213
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b 463 RNDVF8WSSCSROVIANTELSTAGALCLADOPRP 495	PROFIT OF THE PR		288

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28 VETLVVADDKAAAFHGTGLKRYLLTVMAAAAKAFKHPSIRNPVNLVVTRLVILGSGGBGP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 NITANLISSLLSVCGWSQTINPEDDIDPGHADLVLYITRFDLELPDGNRQVRGVTOLGGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 OVGPSAAQTLRSFCTWORGLNTPNDSDPDHFDTAILFTRQDL-CGVSTCDTLGNADVGTV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 CSPTWSCLITEDTGFDLGVTIAHRIGHSFGLEHDGAP-----GSGCGPSGHVMASDGAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347 CDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHDNSKPCTNLNGGG-GSSRHVMAPVMAH 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LELLVAVGPDVFQAHQEDTERYVLTNIANIGAELLRDPSLGAQFRVHLVGWVILTEPEGAP 67
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Nommalia, Butheria Rodentia, Sciurognathi, Muridae, Mutinae, Mus
NCBITTAXID=10090,
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                                                                                                                                                                                                                                                                                                                                                            Ouery Match 25.1%; Score 286; DB 11; Length 845; Bet Local Similarity 32.2%; Pred. No. 3.3e-17. Matches 68; Conservative 28; Manatches 107; Indels Matches 107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 1092 AA, 120324 MW, BSF03956553536AB CRC64,
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SSUORISE, RAM, 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AA. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AA. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AA. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AA. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AA. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A9225 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A925 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A925 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A925 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A925 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A925 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A925 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A925 CRC64, SEDURICE 645 AM. 91239 MM; BASCC119DD1A925 CRC64, SEDURICE 645 AM. 9125 AM. 9125 AM. 9125 AM. 9125 AM. 9125 AM. 9125 AM. 9125 AM. 9125 AM. 9125 AM. 912
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01-948-2003 (TERMELTS) 23, Last sequence update)
10-07-2003 (TERMELTS) 25, Last annotation update)
19pochetical metalloprotesse.
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33.0%; Pred, No. 7.8e-17;
ive 40; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 PRAGLAWSPCSRRQLLSLLSAGRARCVWDPP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   406 VDPEEPWSPCSARFITDFLDNGYGHCLLDKP 436
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STRAIN=CS7BL/6J, TISSUE=Eye;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE, PSSO215; ADAM MEPRO, 1.
PROSITE, PSSO092; TSP1; 4.
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ses 70, Conservative 4
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 QVGPSAAQFLRSFCTWQRGLNTPNDSDPDHFDTALFTRQDL-CGVSTCDFLGMADVGTV 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 NITANLISSLLSVCGWSQTINPEDDIDDFGHADLVLYITRFDLELPDGNRQVRGVTQLGGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 LELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVRAVILTEPEGAP
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Bukaryota, Matazaa, Chordata, Craniata, Vertebrata, Buteleostomi,
Memmella, Butheria, Rodentia, Schurognathi, Muridae, Musinae, Moss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.1%; Score 286; DB 11; Length 833; 32.2%; Pred. No. 3.3e-17;
68; Conservative 28; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2003 (TEBMBLrel. 23, Created)
01-WAR-2003 (TEBMBLrel. 23, Last sequence update)
01-077-2003 (TEBMBLrel. 25, Last annotation update)
A disintegrin-like and metalloprotesse.
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Best Local Similarity
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9: Gans

93, Indels

8; Gaps

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64 EGAPNITANLISSLESVCGWSQTINPEDDIDPGHADLVLYITRFDL-ELPDGNROVRGVT 122

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181 EGL-LINHHADQSINSFCQWQSALVGXXXXRRHDHA---ILLTGFDICSWXXEPCDTLGFA 236
                                       123 QLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPGSGCGPS-GHVMASDGAA 181
                                                                      237 PISCHCSKYRSCTINEDTGLGLAPTIAHESGHNPGWUHDG-BGNPCRKAEGNIMSPILTG 295
                                                                                                                                                                                                                                                                                      C.-WAY.2007 (TERBELEG. 13, Lettered)
C.-WAY.2007 (TERBELEG. 13, Lettered)
C.-CYT.2007 (TERBELEG. 13, Lettered)
COST.2007 (TERBELG. 13, Lettered)
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                                                                                                                                                     296 NNGVFSWSSCSRQYLKKFLSTPOAGCLVDEPK 327
                                                                                                                                                                                                                                                       PRT; 1091 AA
                                                                                                                                                                                                                                                       PRELIMINARY;
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NCBI TaxID=7227;
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FlyBase; FBgn0034778; CG3622. GO; GO:0004222; F:metalloendopeptidase activity; IEA.

286 LFIETAIPVDSDLY-AHMOKNFPTNTESKVVSFLLAMIN-GVQLLXHHPTLGRRINPVLX 343 56 KWILT -- EPEGAPNITANLISSLLSVCGWSQTINPEDDIDPGHADLVLYITRFDLELPD 113 344 RLEINKSWDPPGLVR-SRDVBNYLNSFCKWOEKLNPFSDADPLHYDHALVLTGLDLVTYD 402 114 ---GNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAPGSGCGP 170 403 KGKANSQVVGMATVKGMCTSIYSCTINEAXHFBSVFVVAHBIGHNLGMRHD-AKEISCDP 461 6 IHIBILUANGPDVFQAHQE----DTE----RYVITNINIGAELL-RDPSLGAQFRVHLV SS 171 SGHVMASDGAAPRAG---LAWSPCSRRQLLSLLSAGRARCVWD 210 462 TWHIM----SPKLGSGKVTWSKCSRTYLEDFLMDPQABCLFD 499 completed: March 13, 2004, 07:43:15 Search comp Job time : a à 임 ò a ò

Indels 27; Length 1091;

. Match Local Similarity 32.7%; Pred. No. 5.1e-15; tes 73; Conservative 38; Mismatches 85;

Query Match

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CO) GOODGEORY FIRST FIRST CON HISTORIES 13A.

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Potal number of hits satisfying chosen parameters: 1586107 seqs, 282547505 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

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Sequence 933 AA;

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Query Match

100.04, Score 1141; DB 5; Length 933;

Bost Local Similarity 100.04, Pred. No. 6.6e.10;

Matches 214; Conservative 0; Missacches 0; Indels 0
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198 VTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSPGLEHDGAPGSGCGPSGHVMASDGA 257 VTQLGGACSPTWSCLITEDTGPDLGVTIAHEIGHSPGLEHDGAPGSGCGPSGHVMASDGA 180

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181 APPAGLAWSPCSRROLLSLLSAGRARCVWDPPRP 214 258 APRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRP

44016618 RESULT

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AAO16618 standard, protein; 1297 AA
                                                  AA016618
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40 Human von Willebrand factor (vWF) -cleaving enzyme-related protein Human; protease inhibitor; gene therapy; vWF-cleaving enzyme; no Millebrand Eccor-cleaving enzyme; thrombocytopenic pupura; myocardial infarction; errebral infarction, arteforal infarction, arteforal infarction.

(first entry)

15-MAY-2003

platelet thrombosis, stenosis.

W0200288366-Al. Homo sapiens

25-APR-2001, 2001JP-00128342. 27-JUL-2001, 2001JP-00227510. 28-SEP-2001, 2001JP-00302977. 25-JAN-2002, 2002JP-00501596. 25-APR-2002; 2002WO-JP004141. 07-NOV-2002

Hamamoto T, Nozaki C, (KAGA) CHEMO-SERO-THERAPEUTIC RES INST. Maeda H. Mimura N. Soejima K,

Nakagaki

von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and supplientary therapy for, thrombotto-thrombosytopenic purpura, and for developing drugs oc, e.g., spocardial infarction and cerebral infarction PI; 2003-120479/11. N-PSDB; ABT32584.

4; Page 92-101; 144pp; Japanese Claim 2288888888822

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Sequence 1297 AA;

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                                                               1 AAGGILHLELLVAVGPDVPQAHQEDTERYVLTWLNIGAELLRDPSLGAQFRVHLVKXVIL
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Length 1297;
                              Indels
100.0%; Score 1141; DB 6;
100.0%; Pred. No. 1.1e-109;
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                                 0; Mismatches
                    Best Local Similarity 100.
Matches 214; Conservative
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TEPEGAPNITANLISSLLSVCGWSQTINPEDDIDPGHADLVLYITRPDLELPDGNRQVRG 120 1 AAGGILHIELLVANGPDVPQAHQEDTERYVJTNINIGAELIRDPSLGAQFRVHLVKKVIL 19 61 TEPEGAPNITANLISSLISVOGWSQTINPEDDIDPGHADLVLYITRFDLELPDGNRQVRG 120

181 APRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRP 214 181 APRAGLAMSPCSRRQLLSLLSAGRARCVWDPPRP

AAE24449 standard, protein, 1353 AA

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Human Von Willebrand factor-cleaving protease fragment #2.
04-OCT-2002
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(first entry)

Human, Von Willebrand fector-cleaving protease; VWP-cp) therapy; enzymen transports are accompanied to the companied of the companied of the companied of the companied of the companied of the companied of the companied of the companied of the companied the companied of the comp

W0200242441-A2 Homo sapiens.

10-MAY-2002

20-NOV-2001; 2001MO-EP013391 22-NOV-2000, 2000US-00721254 12-APR-2001, 2001US-0083338

Furlan M, Turecek P, Schwarz Kerschbaumer R, Tagliavacca Laemmle B, Gerritsen HB, F Scheiflinger F, Antoine G, Zimmermann K, Voelkel D; BAXT | BAXTER AG

a a

Novel isolated or substantially purified von Willebrand factor-cleaving concase, useful for producing preparation for threapy of horomoses and phremoedial of disease such as thrombotly to purpure. WPI; 2002-479950/51

Claim 1, Page 64-68, 93pp, English

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invention relates to an isolated or substantially pure Von Willebrand
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Query Match

100.0%; Score 1141; DB 5; Length 1353;
Seet Local Similarity 100.0%; Pred. No. 1.18-1.08

Matches 214; Conservative 0; Mismatches 0; Indels 0;
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AAO16617 standard, protein, 1353 AA 13016617

Human von Willebrand factor (vWF) - cleaving enzyme-related protein (first entry) AA016617;

Human, protease inhibitor, gene therapy; vWF-cleaving enzyme; yon Whitebrand fercor-cleaving enzyme; birochocycogenic purpura, wycardiai infarction; cerebral infarction, arceriocolerosis; platelet thrombosis; stenosis.

domo sapiens

40200288366-AL

25-APR-2002, 2002WO-JP004141. 17-NOV-2002

25-APR-2001, 2001JP-00128342. 27-JUL-2001, 2001JP-00227510. 25-JAN-2002, 2002JP-00017596. 25-JAN-2002, 2002JP-00017596.

(KAGA) CHEMO-SERO-THERAPEUTIC RES INST. Soefima K.

Hamamoto T, Nakaqaki T; Nozaki C. Maeda H. Mimura N.

2003-120479/11. WPI: 2003-120479/ N-PSDB: ABT32583.

von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and audicementy therespy for, forembotic thrombotic thrombotic and condevoloping drugs for e.g. mycoardial infarction and cerebral infarction.

Claim 4, Page 82-92; 144pp; Japanese.

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ABB04153

181 APRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRP

ABB04153 standard; protein, 1416 Ah Human ADAMTS-M polypeptide. (first entry) 26-MAR-2002 ABB04153:

cochesi aliasasi anthan, Albahasari aliasasi organ transplant rejection, cabania, aliaseyi cancer, Joukamaa, Ivyphoma, Garappoonis, cabania, aliaseyi cancer, Joukamaa, Ivyphoma, Garappoonis, and Antonio anterior companie, organis, and benefi aliaser, organis, and anterior concerning the personnel organism organism and anterior concerning the personnel Ostecarthritis; rheumatoid arthritis; inflammatory bowel disease;

Location/Qualifiers Homo sapiens

Peptide

/note= "The mature form of the ADAMTS-M protein is processed by furin cleavage of the prodomain" 'label= Furin_cleavage_site label= Prodomain .1416 Cleavage-site

/label= Mature ADAWTS-M protein /note= "The mature form of the ADAWTS-M protein is processed by furin cleavage of the prodomain"

Protein

394 424

Domain Domain Domain Dотаin Domain PFIZ) PFIZER PROD INC WPI; 2002-084275/12.

P1152055-A1 07-NOV-2001 N-PSDB; ABA02549.

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218 VIQLGGACSPIWSCLITEDIGFDLGVILAHBIGHSFGLEHDGAPGSGCGPSGHVMASDGA 277
VTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLRHDGAPGGGCGPSGHVMASDGA 180
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Scheiflinger F, Antolne G, Kerschbaumer R, Tagliavacca L;
Zismernan K, Voelkel D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Von Willebrand Eactor-cleaving protease (vWF-cp)
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|note= "Thromspondin type I motif"
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/noces "Thromspondin type I motif"

1075. 1131

/noces "Thromspondin type I motif"
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/note= "Thromspondin type I motif"
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1877. .439
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12-APR-2001; 2001US-0083328
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Query Match Best Local Similarity Matches 214; Conserv Sequence 1416 AA;

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Local Similarity
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conducting a purified human aggrecanase protein which can be used to 
develop inholitors of aggrecanase.
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Wolfman N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14: SEC ID NO 8: 24pp: English.
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Agostino MJ,
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Best Local Similarity 100.
Matches 214, Conservative
Twine NC,
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Homo sapiens

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13-JUN-2002
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08-DEC-2000; 2000US-0254399P. 21-DEC-2000; 2000US-0257803P. 05-JAN-2001; 2001US-0260110P. 19-JAN-2001; 2001US-026281P. 25-JAN-2001; 2001US-0264629P. DS-DEC-2001; 2001MO-US046964.

INCY-) INCYTE GENOMICS INC

LATE G. WALLAR MY, RAGALLICK DA. Banghan WB. Griffith JAA. Searnakar Ay LATE G. WALLAR MY. RAGALLA MA. GARDAL AR. MA. YOUNG J. Elloret WS. REMNUMEN J. THANGEWELK L. M. Y. WARTER DA. LA DAW. LEE EA. REMOUNDLEY CW. ATVIETS C. Delegeates AW. You MG, KEAN FA, I. Sanjanwala MM;

MPI; 2002-519664/55. N-PSDB; ABQ75946.

useful New isolated Protein Modification and Maintenance polypeptides, for diagnosis, and treatment of e.g. gastrointestinal disorders.

Claim 1 (a); Page 154-157; 200pp; English.

The investion relates to an inclused perstativ Modification and Maintenance (1994) golypeptides for the investion may be used in the diagnostic research and personate for the investion may be used in the diagnostic research and personate for the investion may be used in the diagnostic research and personate for the investigation of activity of 1996. These includes gentrointential Modernates of Thomas (1996) and the includes the includes of the investigation of the includes of the investigation of the includes the includes of the investigation of the include of the investigation of the include of the investigation of the include of the investigation of the investigation of the investigation of the investigation which has been course to equal compared on the state of the investigation which has been course to equal compared to the investigation of the investigation which has been condition to have become one protection and maintenance and confidential the been found to have become one protecting and include and the investigation of the investigation which has been found to have become one protecting and maintenance and confidential the been found to have become one protecting and maintenance and confidential the been found to have become one of the investigation with the been found to have broadless that it is the surface of protecting and the confidence of protecti

ó 100.0%; Score 1141; DB 5; Length 1445; 100.0%; Pred. No. 1.2e-109; atlve 0; Mismatches 0; Indels 0; Query Match Best Local Similarity 100. Matches 214, Conservative Sequence 1445 AA,

78 AAGGILHLBLLVAVGPDVFQAHQEDTERYVLTNINIGAELLADPSLGAQFRVHLVKNVIL 137 1 AAGGILHLELLVAVGPDVFQAHQEDTERYVLTNLNIGAELLRDPSLGAQFRVHLVKKVIL

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61 TEPEGAPNITANLISSILSVCGWSQTINPEDDIDPGHADLVLYITREDLELPDGNRQVRG

198 VTQLGGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAFGSGCGPSGHVMASDGA 257 181 APRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRP 214 258 APRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRP Ą AAO16621 standard, protein, 312 AA016621; RESULT AA01662 ò g

(first entry)

.5-MAY-2003

Human von Willebrand factor (vWF) -cleaving enzyme-related protein

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Numen, procease inhibitor, gene therapy, vwP-cleaving enzyme, von Alliebrand factor-cleaving enzyme, thrombocycopenic puppura, ayocardial infarction, cerebral infarction; arteriosclerosis, placeler thrombosis, senosis.

W0200288366-A1. Homo sapiens.

07-NOV-2002

25-APR-2002, 2002WO-JP004141

25-APR-2001; 2001JP-00128342. 27-JUL-2001; 2001JP-00227510. 28-SEP-2001; 2001JP-00302977. 25-JAN-2002; 2002JP-00017596 Maeda H, Nozaki C, Mimura N, Soelima K,

KAGA) CHEMO-SERO-THERAPEUTIC RES INST

Hamamoto T, Nakagaki WPI: 2003-120479/11.

von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and pupplementary therety for, thrombotic informboropenic puppra, and dover developing drugs for e.g. mycoardial infaction and carebral infaction N-PSDB, ABT32587.

Claim 4; Page 121-123; 144pp; Japanese

The invention comprises the amino acid and coding agentesce of a von Willebrand Scotor (very) -clearing arrayme. The DNA and procein sequences of the invention are useful. In the dispussion and treatment of cital interaction operations and treatment of cital interaction operations and treatment of cital and except a feet interaction are settled and the contraction of the interaction of the

Sequence 312 AA;

1 AAGGIIHLELLVAVGPDVFQAHQEDTERYVLTNINIGAELLRDPSLGAQFRVHLVKWYIL Gaps ö Score 1065, DB 6, Length 312, Pred. No. 1.3e-102, 4; Indels 0; Mismatches 93.3%; datches 202; Conservative ery Match

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Gaps

TEPEGAPNITANLISSLLSVCGKSQTINPEDDIDPGHADLVLYITRFDLELPDGNRQVRG 120 AAGGILHLELLVAVGPDVPQAHQEDTERTYLTKLNIGAELLRDPSLGAQPRVHLVYOWIL 61

9

TEPEGAPNITANLISSILSVCGWSQTINPEDDIDPGHADLVITAFDLELPDGNRQVRG 120 VTQLGGACSPTWSCLITEDTGFDLGVTANEIGHSFGLEHDGAPGSGCGPSGHVWASDGA 180 21

181 APRAGLAWSPCSRROLLSLLSAGRAR 206

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121 VTQLGGACSPINSCLITEDIGFDLGVTIAHEIGHSFGLEHDGAFGSGCGPSGHVMASDGA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, protease inhibitor; gene therapy; vMF-cleaving enzyme;
row Millebrand Entor-cleaving enzyme; thrombocytopenic purpura;
myocardial infarction; cerebral infarction; arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                          181 APRAGLAWSPCSRRCLLSLLRTGALR
                                                                                                                                                                                                                                             AA016619 standard; protein; 1378 AA
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27-JUL-2001, 2001UP-00227510.
28-SEP-2001, 2001UP-00302977.
25-JAN-2002; 2002UP-00017596.
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N-PSDB; ABT32585.
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Nillabeard Second VWF)-Cleaving enzyme. The DNA and protein sequence 
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vM filabrand factor-cleaving enzyme; thrombocytopenic purpura;
nyocardial infarction; oerebral infarction; arteriosclerosis;
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181 APRAGLAWSPCSRRQLLSLLSAGRAR 206
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27-JUL-2001; 2001JP-00227510.
28-SEP-2001; 2001JP-00302977.
25-JAN-2002; 2002JP-00017596.
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cartilage; osteoarthritis; inflammatory disease; enzyme.
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100.0%; Pred. No. 6e-102;
.ive 0; Mismatches 0;
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181 APRAGLAWSPCSRRQLISLL----RPV--PPSP 207
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sillabrand statoor /verby-cleaving ensure. The DNA and protein sequences of
the invention are useful. In the disposite and treatment of cital
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and suppleementary therappy for, intrombotto thrombotto repento purpura, and for developing drugs for e.g. myocardial infarction and cerebral infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TEPEGAPNITANLISSLISVCGWSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human von Willebrand factor (vWF)-cleaving enzyme-related protein #9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            von Willebrand factor-clearing enzyme; thrombocytopenic purpura; myocardial infarction; cerebral infarction; arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease inhibitor; gene therapy; vWF-cleaving enzyme;
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Pred. No. 3.8e-102;
0, Mismatches 2; Indels
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2001JP-00227510.
2001JP-00302977.
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N-PSDB; ABT32588.
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Best Local Similarity
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WO200288366-A1.

07-NOV-2002

Homo sapiens

Human;

AA016622;

25-APR-2001; 2 27-JUL-2001; 2 28-SEP-2001; 2 5-JAN-2002,

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New anti-anglogenic intestinal polypeptides, zdints polypeptides, which are mades of distincipglin proceases, for modulating extracellular matrix integraction, tumor supplession and wound healing.
                                                                                                                                            42 AAGGILHLELLUANGPDVPQAHQEDTERYVLTNLNIGAELLRDPSLGAGFRVHLVKWYIL 101
                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a human relief polypoptide. The diffits of properties is an anti-majogenic insertial polypoptide admiss is used for modificing extracellular matrix interactions. Edites polypoptide used to the control as a tool for identifying new faith, mambers of polypoptides. Editis polymorications are useful as probes of properties.
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exceedilist matrix interaction; tunnor suppression; genera emutation;
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Mismatches
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polociding a purified human aggrecanase protein which can be used to 
develop inhibitors of aggrecanase.
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Morris SA

Wolfman N,

Agostino MJ,

Racie LA, Twine NC, WPI; 2003-801251/75

N-PSDB; ADD94032, ADD94033.

AMHP) AMERICAN HOME PROD CORP.

25-JAN-2002; 2002US-00057487. 16-OCT-2001; 2001US-00978979,

JS2003105313-A1. uman; enzyme.

55-JUN-2003

claim 13, SEQ ID NO 1, 24pp, English.

Human aggrecanase protein partial amino acid sequence.

(first entry)

29-JAN-2004

ADD94031, ADD94031

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ADD94031 standard, protein; 242

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Length 242;

92.6%; Score 1057; DB 7; 100.0%; Pred. No. 6e-102;

Query Match Best Local Similarity Sequence 242 AA;

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0; Gaps Query Match 99.7%; Score 1046; DB 4; Length 203; Bert Local Similarity 99.5%; Pred. No. 6.6e-101. Natches 197; Conservative 1, Mismarches 0; Indels 1 Sequence 203 AA;

181 APRAGLAMSPCSRROLLS 198

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Search completed: March 13, 2004, 07:39:01 Job time : 32.3198 secs 182 APRAGLAWSPCSRRQLLS 199

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Parent No. 932/00104041641 404985712
Parent No. 932/00104041641 404987108
Parent No. 932/00104041641 404987108
Parent No. 932/0010404108
Parent No. 932/001040419
Parent No. 932/0010419
Parent No. 932/0
                                                                                                                        255 APRAGLAMSPOLLSLISAGRARCVWDPPRP 288
181 APRAGLAWSPCSRRQLLSLLSAGRARCVWDPPRP 214
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75 AAGOLLHLELLVAVGPDVPQAHQEDTERYVLTNINIGAELLRDPSLGAQFRVHLVKAVIL 134

SOFTWARE: Patentin Ver. 2.1 ORGANISM: Human ENGTH: 1416 US-09-836-712-2 TYPE: PRT SEQ ID NO 2

1 AAGGILHLBLLVAVGPDVPQAHQEDTERYVLTWLNIGAELLRDPSLGAQFRVHLVKAVIL 60 ő Ouery March 100.0%; Score 1141; DB 9; Length 1416; Best Local Similarity 100.0%; Pred. No. 5.4e-108 Natches Natches 0; Indels 0; Marches 0; Indels 0;

Gaps

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RESULT 3

We plus 222 Agentice 2, Application US/1022234
Publication No. US/2020304711641
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Publication No. US/2020304711641
APPLICANT LEWY AMAPRIX Once and Proteins and Variance, and Uses Thereof TITIZE ON UNIVERSITY, DAYS 2020-064-16, AVAILABLE TITIZE ONCE TITIZE ONCE AUGUST TO A SUPPLICATION NUMBER: US/202-234
PUBLICATION NUMBER: US/202-234

TYPE: PRT

) ORGANISM: Homo sapiens US-10-222-334-2

1 AAGGILHEBLUVAVGPOVGPOTGBTERYVLTNINIGAELERDPSLGAGFRVHLVKKVLTL Ouery Match 100.0%; Score 1141; DB 1; Length 1427; Best Local Similarity 100.0%; Pred No. 55-108; Score 18 Matches 51, Conservative 0; Mismarches 6; O; Indes 0; Matches 11, Conservative 0; Mismarches 6

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Seguence 8, Application Us/10051487
Publication No. USZOJO105313A
APPLICATE WHEN
TILL OF UNEXTUCH AGREGATION A RIOR APPLICATION NUMBER: 60/241,469 RRIOR FILING DETE: 2000-10-18 NUMBER OF SEQ ID NOS: 8 SOFWARE: Patentin version 3.1 SEQ ID NO 8 ORGANISM: homo sapiens US-10-057-487-8 US-10-057-487-8 TYPE: PRT

1 AAGGILHLELLVAVGPDVFOAHOBDTERYVLTNLNIGAELLRDPSLGAQFRVHLVHMVIL Gaps ., Query Match 100.0%; Score 1141; DB 14; Length 1427; Gert Local Similarity 100.0%; Pered. No. 55-108. Sector Matches 214; Conservative 0; Mismatches 0; Indels 0;

75 AAGGILHLELLVAVGPDVPQAHQEDTERYVITNIAIGAELLRDPSIGAQFRVHLVRAVIL 134

GENERAL INFORMATION:
APPLICANT: Recie, Lisa, A.
Twins, Natalie, C.
Agostino, Michael, J. Sequence 1, Application US/09978979 Patent No. US20020151702A1

US-09-978-979-1

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COMPUTER: STATES
COMPUTER: REAL
SOFT-MEDICATION DATA:

APPLICATION NUMBER: US/09/978,979
FILIND DATE: 16-Oct-2001
CLASSFICATION: <unknown>
PRICR APPLICATION DATA: APPLICATION NUMBER: US/60/241,469

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Bost Local Similarity 99-54; Pered. No. 2.28-99; Length 203;
Matches 197; Conservative 1; Mismatches 0; Indels
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PLIE OF INVESTIVENCE: 59-52.
Best Local Similarity 100.0%; Pred. No. 2.18-100;
Matches 200; Conservative 0; Mismatches 0;
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Patent No. US20020142439A1
GENERAL INFORMATION:
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, ORGANISM: Homo sapiens
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Matches 200; Conservative 0, Mismatches 0, Indels
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US-09-978-979-1

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92.6%; Score 1057; DB 14; Length 242;

ORGANISM: Homo sapiens US-10-057-487-1 Query Match

ASSECTATION OF THE STATE OF THE

US-10-057-487-1 "Sequence 1. Application US/10057487) Publication No. US20030105313A1 ; GRNERAL INFORMATION:

CURRENY PEDILANDAN MUNERS: US/09/781,0808 CURRENY PILING DATE: 2002-01-30 NUMBER OF SEQ ID NOS: 122 SOCTWARE: PARSEC for Windows Version 3.0 SEQ ID NO: 11 ENGTH: 1120

PERTURN NAME/KEY: VARIANT LOCATION: (1)...(1120) OTHER INFORMATION: Xaa = Any Amino Acid US-09-781-0808-11

TYPE: PRT ORGANISM: Homo sapiens

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61 TEPEGAPNITANLISSILSVCGWSQTINPEDDIDPGHADLVLYITRFDLELPDGWRQVRG 120
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Patent No. US20020136713A1
GENERAL INFORMATION:
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Scheiflinger, Friedrich
Antoine, Gerhard
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; Patent No. US20020136713A1
; GENERAL INFORMATION:
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Tagliavacca, Luigina
Zimmermann, Klaus
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APPLICANT: Schearz, Hans Peter
APPLICANT: Scheafflinger, Fried
APPLICANT: Antoine, Gerhard
APPLICANT: Kerschbaumer, Rand
APPLICANT: Tagliavacca, Luigii
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δ QQ. US-09-833-328-4

CIPRENT APPLICATION NUMBER: UJ/09/833,328
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 09/71,254
NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 3.1

) ORGANISM: human US-09-833-328-4 SEQ ID NO 4 LENGTH: 148

TYPE: PRT

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8 LELLVANGPDVFQAH-QEDTERYVLTMINIGABILRDPSLGAQFRVHLVKMVILTEPEGA 66
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31.6%; Score 361, DB 11, Length 997;
Best Local Smilarity 38.4%; Pred, No. 5.8e.28

Matches B1; Conservative 35; Mismatches 97; Indele 6
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APRICANT: Gorman, Linda
TITLE GO FUNKENTON: Forceits and Nucleic Acids Encoding Same
TITLE REFERENCE: 2140-2-168
CURRENT PARLICATION NUMBER: US/09/981,151A
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Shinkete, Richard A
Pedigan, Maralithara
Goo, Xiaojia
Petturasian, Neera
Tunjier Jr, Raymond
Burges, Cathorine E
Rethusen, Bryan
Server, Kaneeh
Syrek, Kimberl, A
Gampolli, Esha
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Pertanathee, Esha
121 ITEDIGEDIGWII 133
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US-09-981-151A-32
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Beet Local Smilarity 100.0%; Prod. No. 1.2e-65;
Metches 136; Conservative 0; Mismatches 0; Indels
                              CURRENT APPLICATION WASHER US (9/633,1288 CURRENT APPLICATION WASHER US (9/721,224 FRICE FILLING DATE, 2001-04-122 MANNER OF SEQ ID NOS: 15 SOTTAMES: Partic Newsign OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEQ ID NOS: 15 LEAVED THE US APPLICATION OF SEC ID NOS: 15 LEAVED THE US APPLICATION OF SEC ID NOS: 15 LEAVED THE US APPLICATION OF SEC ID NOS: 15 LEAVED THE US APPLICATION OF SEC ID NOS: 15 LEAVED THE US APPLICATION OF SEC ID NOS: 15 LEAVED THE US APPLICATION OF SEC ID NOS: 15 LEAVED THE US APPLICATION OF SEC ID NOS: 15 LEAVED THE US A
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Patent No. US20020136713A1
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Best Local Similarity 100.(
Matches 133, Conservative
       FILE REPERENCE: 247.00CIP
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ORGANISM: human
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LENGTH: 133
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US-09-833-328-2
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183 RAGLAWSPCSRRQLLSLLSAGRARCVWDPP 212
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Job time : 17.9417 secs
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304 IXITHHADNILKSECKWOKSINWKGDAHPLHHDTAILLTRKDL-CAAMREPCETLGLSHV 362
                                                                                                          125 GGACSPTWSCLITEDTGFDLGVTIAHEIGHSFGLEHDGAFGSGCGPSG---HVWASDGAA 181
                                                                                                                                                               363 AGMCQPHRSCSINEDTGLPLAFTVAHELGMSPGIQHDGS-GNDCEPVGKRPFIMSPQLLY 421
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31.6%; Score 361; DB 15; Length 1686;
Bost Local Smilarity 38.4%; Fred. No. 1.28-27;
Matches 81; Conservative 35; Mismatches 97; Indels 8;
                                                                                                                                                                                                                                                                  182 PRAGLAWSPCSRRQLLSLLSAGRARCVWDPP 212
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Publication No. US20040006016A1
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ORGANISM: Homo Sapien
US-10-386-414-2
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68 NITANLISSLISVCGMSQTINPEDDITDPGHADLVLYITRPDLELPDGNR--QVRGVTQLG 125
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963 AGMCQPHRSCSINEDTGLPLAFTVAHELGHSFGIQHDGS-GNDCEPVGKRPFIMSPQLLY 421
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                                                                                                                                                                                                                                                                                     122 DAAPLTWSRCSRQYITRFLDRGWGLCLDDPP 452
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Patent No. US20020110894A1
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US-09-918-171A-7
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Gencies version \$1.6 Copyright (c) 1359 - 2004 Compugen Ltd. Ow procein - protein mearch, using www. and own the angle of the angle o	er of h seq le seing:	Dischass : I stoned foreits Ask 120, COUR per : 1 (7997 (Stocias Ask	Amount Common March Longish Do 10 10 10 10 10 10 10 10 10 10 10 10 10

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                                                                 114 GNRQVRGVTQLGGACSPTWSCLITEDTGFDLGVTLAHEIGHSFGLEHDGAPGSGCGPSGH 173
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                                                                                                                                                        219 G---TLGLASVAGMCEPERSCSINEDIGLGSAPTIAHEIGHNFGMNHDGI-GNSCGTKGH 274
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CURRENT FILING DATE: 2000-12-08
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CURRENT FILING DATE: 2000-12-08
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PRIOR FILING DATE: 1299-12-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PASESEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US 60/169,769
PRIOR FILING DATE: 1999-12-09
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Friedrich, Glenn
Scoville, John
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Patent No. 6649399
GENERAL INPORMATION:
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Patent No. 6649399
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Sands, Arthur T.
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 507
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APPLOANT, Embedvet Britan
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CHERRY PRELICATION STREET WAS 100-508.
CHERRY PRELICATION STREET WOULD STREET WAS 100-508.
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FRIDE PRILICATION STREET WAS 100-508.
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28.5%; Score 325.5; DB 4; Length 356; Bet Local Similarity 36.4%; Pred. No. 346-27; AB-276.3 No. 346-27; Indels 25. Matches 82; Conservative 36; Mismatches 82; Indels 25.
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CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/169,769
PRIOR FILING DATE: 1999-12-09
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SOFTWARE: PastSEQ for Mindows Version 4.0
SEQ ID NO 22
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Patent No. 6649399
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ORGANISM: Homo sapiens
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US-09-963-791-20
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Best Local Similarity
Matches 82; Conserv
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TYPE: PRT
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GARBEAL INTERMENTION.
APPLICANT. TOWNER, C. Alexander Jr.
APPLICANT. TOWNER, C. Alexander Jr.
APPLICANT. TOWNER, C. Alexander Jr.
APPLICANT. SECURITY. CARRET C. Alexander Jr.
APPLICANT. SECURITY. SOUTH C. Alexander Jr.
APPLICANT. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURITY. SECURI
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TO ACCUSE THE DESCRIPTION OF ACCUSE AND POLYMUIGHCEGES ENCOLING THE PROPERTY HILDS. TO ACCUSE AND ACCUSE AND ACCUSE AND ACCUSED AND ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED ACCUSED A
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27.04; Score 307.5; DB 4; Length 1224;
Best Local Similarity 36.24; Pred. No. 199-24;
Matches 77; Conservative 35; Mismatches 92; Indels 9;
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28.5%; Goore 325.5; DB 4; Length 908;
Best Local Similarity 36.4%; Pred. No. 146-26;
Marches 82; Conservative 36; Masmatches 82; Indels 25
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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CURRENT FILLIN DATE: 2000-12-08
PRICES APPLICATION NUMBER: US 60/169,769
PRIOR FILING DATE: 1999-12-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 4, Application US/09930872
Patent No. 6448388
                                                                                                                                                                                                                                 Sequence 2, Application US/0963791
Patent No. 6649399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Homo sapiens
US-09-963-791-2
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APPLICANT TURRE, C. Alexander Jr.

APPLICANT TURRE, C. Alexander Jr.

APPLICANT TURRE, C. Alexander Jr.

APPLICANT Exabled E. Brin

APPLICANT, Exabled E. Brin

APPLICANT, SAMES ATELUT.

TITLE OF TURRETRON: LEX. OLGS - USA

TITLE OF TURRETRON E. LEX. OLGS - USA

TITLE APPREDICATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 PNITAN--LISSLLSVCGMSQTI---NPEDDTDP----GHADLVLYITRFDL----ELPD 113
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28.5%; Score 325.5; DB 4; Length 589;
Matches Banilarity 36.4%; Pred. No. 7.28-7.
Matches 82; Conservative 36; Mismatches 82; Indels 25; Gaps
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28.5; Score 325.5; DB 4; Length 757;
Best Local Similarity 36.4t; Predt. No. 1e-26;
Matchae 82; Conservative 36; Mismatchae 82; Indela 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .74 ----VMASDGAAPRAGLAWSPCSRRQLLSLLSAGRARCV-WDPPR 213
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NUMBER OF SEQ ID NGS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
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CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/169,769
PRIOR FILING DATE: 1999-12-09
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6649399
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CURRENT APRILON DAYE: 1999-09. US/91.130,491
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Best Local Scinlarity 25.7%; Score 304.5; DB 4; Length 349;
Best Local Scinlarity 29.8%; Pred No. 2.9e-24; Indels 19;
Matches 65; Conservative 40; Masches 94; Indels 19;
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APPLICATIVE, VUM Mart.; Harold
THILE OF INVESTIGATION: Human Application to the condition of the condition of the same and investigation to the condition of the same application of the condition                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L78 --DGAAPRAGLAWSPCSRRQILSLLSAGRARCVWDPPR 213
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tive 40; Mismatches 94;
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SOFTWARE: FastSEQ for Windows Version 3.0
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EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: US 60/054,961
EARLIER FILING DATE: 1997-08-06
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; Sequence 2, Application US/09130491
; Patent No. 6416974
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US-09-568-559-2
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                                                                                                           GAPNITANLTSSLLSVCGWSQTINPEDDIDFGHADLV--LYITRFDLELFDGNRQVRGVT 122
                                                                                                                                                                                                                                                                                                                                                                                         50 PGLVISHHADHILSSPCQMQSGLMGKDGTRHDHAILLTGLDICSWRNEPCD----TLGFA 405
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                          LHIBLIVAVGPDVPQAH-QEDTERYVLTNINIGABLIRDPSLGAQFRVHLVKKVILTEPE 64
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PRIOR PRING DATE: 1997-06-03
WIMBER OF SEQ 1D NOS: 14
SOFTWARE Patentin Version 3.0
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Patent No. 6565858
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Patent No. 6649377
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APPLICANT: Klonowski, Paul
APPLICANT: Allard, John
APPLICANT: Heller, Renu
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Matches 65, Conserv
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APPZICANT: Muon, Kunji
171E 60 HVNRNICHS HOMBA ADANTS-1 procein, gene encoding the same, pharmaceutical
171E 100 PROFINICHS (composition and method of immunologically analyzing human ADAM
File RESERVENCE (07092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  78; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                    Query Match 26.4%; Score 301; DB 4; Length 468; Best Local Similarity 36.5%; Pred. No. 2.4e-2%; Matches 79; Conservative 32; Mismatches 78; Indels 3
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CURRENT FILING NETE: 1999-12-03
ENIOR APPLICATION NUMBER: UP 9-160422
PRIOR FILING DATE: 1997-06-03
NUMBER: OS SEQ 10 MOS: 14
NUMBER: CS EACH 10 MOS: 14
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US-09-963-791-6
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                                                         LENGTH: 468
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                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 PNITAN--LISSLLSVCGWSQTI---NPEDDTDP----GHADLVLYITRFDL----ELPD 113
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376 GIVCDPSRSCSVIEDDGLQAAFITAHELGHVENMPHDDAXQCASLNGVNQDSHP0ASSMLS 435
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26.4%; Score 301; DB 4; Length 317;
Bet Local Similarity 36.5%; Pred. No. 1.4e-34
Matches 77; Conservative 32; Mismatches 78; Indels 2
                                                                                                                                                                           178 --DGAAPRAGLAWSPCSRRQLLSLLSAGRARCVWDPPR 213
                                                                                                                                                                                                                                                                       436 NLDHSOP----WSPCSAYMITSFLDNGHGECLMDKPO 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 ----VMASDGAAPRAGLAWSPCSRROLLSLL 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 25
SECTIARS: RestSEQ for Windows Version 4.0
SEQ ID NO 16
IENCTH: 317
IENCTH: 317
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Patent No. 6649399
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Patent No. 6649399
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281 YVEVLVVADTXMYEYHGRSLEDYVLTLFSTVASIYRHQSLRASINVVVVKLIVLXTENAG 340 67 PNITANLTSSILSVCGMSQTINPEDDTDPGHADLVLYITRFDLELPDGNRQVRGVTQLGG 126 341 PRITQNAQQTLQDFCRWQQYYNDPDDSSVQHHDVAILLTRKDICRSQGKCDTLGLAELGT 400 127 ACSPIWSCLITEDIGFDLGVTIAHEIGHSFGLEHDGAPGSGCGP------ 170 401 MCDMQKSCAIIBDMGLSAAFTIAHBLGHVFSIPHDDB--RKCSTYMPVNKVCKFQSTKFD 458 7 HIELLUANGPDVFQAHQEDTERYVLTNINIGAELIRDPSLGAGFRVHLVROVILTEPEGA 66 Ouery Match 25.94, Score 255; DB 4; Length 2165, Bet Local Similarity 3.44, Pred. Mo. 1e-25, Bet Local Similarity 3.40, Franches 104, Indels 26; Gaps Matches 79; Conservative 3.0, Mismatches 104, Indels 26; Gaps è g à

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Search completed: March 13, 2004, 07:46:06 Job time : 10.0281 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. - protein search, using sw model OM protein Run on:

March 13, 2004, 07:33:19 ; Search time 2.4776 Seconds | Withbour alignments | 2756:533 Willion cell updates/sec

399 1 PGLYYSANBQCRVAFGPKAV......VPLLDGTBCGVEKWCSKGRC 71 US-09-836-712-2_COPY_324_394 Title: Perfect score: Scoring table: Seguence:

283366 segs, 96191526 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:* 1: piri:* 2: piri:* 3: piri:* Database

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Result

Description	procellagen N-endo		dene ADAMIS-1 prot		hypothetical prote			vascular apoptosis	hypothetical prote	hypothetical prote	monocyte surface a	probable secretion	E2 protein - human	gene 70 protein -	metalloproteinase	metalloproteinase	probable zinc meta	hypothetical prote	sperm surface prot	phage-related prot	feruloyl-CoA synth	disintegrin and me	low-density lipopr	hypothetical prote	metallothionein A	probable H+-transp	complement C8 alph	ce pr	14
a	T18517	T22836	T00017	T47158	T21371	T00355	T18856	JC7530	T16892	T15976	A60385	B83127	836529	834574	848169	A59414	T37819	T26644	\$23403	C82775	F87297	JC7850	JE0315	T27283	A25775	T06538	CSHUA	500834	T21175
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Match Length	1205	808	951	550	2165	837	1444	610	860	957	826	471	384	145	549	419	512	1042	357	425	969	655	1113	1620	64	561	584	360	651
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ALIGNMENTS

Proceedings on Standard Control and Contro

1 PGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 60 Gape ŝ ch 33.8%; Score 135; DB 2; Length 1205; Length 1205; Length 1205; Length 1205; Second 15; Nismatches 32; Indels 23, Congervative 5; Mismatches 32; Indels 2 Local Similarity Query Match Best Local Si Matches 32;

476 PCLHYSMANEQCREDFOLGYMACTAFRT-FOPCKQLWC-SHPDNPYFCKTKKGPPLDGTWC 533 534 APGKHCFKGHC 544 61 GVEKWCSKGRC 71 à a

Nypotherical procein 15737-4 - Casnorhabditis elegans C.Species (archabditis elegans C.Dates 15-oct 1999 Seepasing Servision 15-Oct 1999 Steat_change 15-Oct 1999 S.Acessack T72356 RESULT 2 T22836

submitted to the EMBL Data Library, June 1996 A.Reference number: 219623 A.Accession: T22836

A.Sistatus: prof.inhary translated Eroco (BPMEL/DDBJ A.MORGONE type: DNA A.MORGONE type: DNA A.MORGONE type: DNA A.MORGONE type: DNA A.MORGONE Type: DNA A.C.TORE TYPE: DNA A.C.TORE TYP

A,Experimental source: clone F57B7 C,Genetics:

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                                                 1 PGLYYSANEÇÇRVAFGPKAVAÇIFAREHLDMCQALSÇHTDPLDQSSÇSRLLVFLLDGTBÇ 60
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Special Caenorhabditie elegame

C,Date 1550-00c-1399 steparec_revision 15-Oct-1999 ftext_change 29-Oct-1999
RRGAJAGEN, S2,3717; 724996
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F:519-575/Domain: thrombospondin type 1 repeat homology <THR3>
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A,Residues: 1-837 <ISH>
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Experimental source: strain 1295VJ
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29.9%; Score 119.5; DB 2; Length 550;
Bet Local Similarity 36.6%; Pted, No. 13e-05;
Matches 26; Conservative 3; Matches 39; Indels 3;
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Pred. No. 1.2e-05;
4; Mismatches 38; Indels 3;
                                                                                                                                                                                                                                                                                                                            Query Match 31.2%; Score 124.5; DB 2; Length 508; Bet Local Similarity 34.6%; Pred No. 3.2e-06; Marches 7:; Conservative 8; Mismatches 30; Indels 13;
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C;Superfamily: thrombospondin type 1 repeat homology <714/3>
F;542-98/Domain: thrombospondin type 1 repeat homology <714/3>
A.Gene: CESP:F57B7.4
A.Map poses: 45,03: 137/2; 221/2; 256/2; 306/2; 409/3; 451/3
A.Interpose: 45,03: 137/2; 221/2; 256/2; 306/2; 409/3; 451/3
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A/Roleule type: DNA
A/Residues: 1-951 «KNA»
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Best Local Similarity 36.6%;
Matches 26; Conservative 4
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A:Gene: ADAMTS-1

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C;Comment: This protein, as a homodimeric protein, belongs to snake venom metalloprotes a a specific unbarrate, induces apoptosis in vascular endothelial cells.
C;Gemeitos:
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A; Experimental source: strain Bristol N2
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                                                                                                                                                                                                                                                                                                                                                                                                       9 EQCRVARGEXAV---AC-TFARE--HLDMCO-----ALSCH------TDPLD 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nygochetical process; TSD2.1 - C.enorrhabditis elegans
C.poness: Camporthabditis elegans
C.poness: 20-8p1199 #eequence_revision 20-8ap-1999 #text_change 20-8ap-1999
C.poness: 20-8p1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phypotherical protein Fored: . Caemorhabditis elegans
C.Species Caemorbalis elegans 2599
C.Species:On-Gers-1999 Resquence_revision 20-Sep-1999 #text_change 20-Sep-1999
C.Accession-Ganni 115976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.7%; Score 74.5; DB 2; Length 860; 27.3%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.4%; Score 73.5; DB 2; Length 957;
                                                                                                                                                                                                                                                                DB 2; Length 610;
                                                                                                                                                                                                                                                                                                                                26; Indels
                                                                                                                         Aldene: vapl.
Vyperiamily: mouse meltrin alpha; disintegrin homology
C:Ksywords: apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bentley, D.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid T19D2.
A;Reference number: Z18599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: The sequence of C. elegans cosmid F08C6. A; Reference number: 218440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       569 KNPCNIYYSPNDEDKGMVLPGTKCADRKACSNGQC 603
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A.Moleorie type: DNA
A.Residues: 1-957 <BRN>
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A;Molecule type: DNA...
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                                                                                                                                                                                                                                                                                                   0.57;
                                                                                                                                                                                                                                                         Query Match
19.5%; Score 78; us.
Best Local Similarity 27.4%; Pred. No. 0.57.
Matches 26; Conservative 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                417 LEGTYCGFGMICROGOC 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: CESP:T19D2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: T16892
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                                                                                                                                                            9
                                                                                                                                                                                                       13.9 PGKDYDADROCOLLTPGPDSRHCP---GLPPPCAALMCSGHLMGHAMCGTKHSPWADGTPC 495
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A;Cross-references :MEBL;550004; PIDN:CAM90293.1; GSPDB:GN00228; CESP:C0284.1
A;Reportisental source: close c028
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Altones-references: EMBLI 250006; PIDN:CAA90302.1; GSPDB:GN00028; CESP:CO2B4.1
A)Experimental source: clone 10705
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Cispociesi Camochabditis elegans
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R. Modurray, A. M. S. 17453
P. Robertray, D. A. S. 17453
                                                                                                                                                            1 PGLYYSANEQCRVARGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC
                                                                                            3, Gaps
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              Score 107.5; DB 2; Length 837;
Pred. No. 0.0004;
7; Mismatches 36; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A,Residues: 240-251;274-283;378-385;507-519 <MA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Mismatches
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ch 26.9%; 1 Similarity 35.2%; 25; Conservative

Query Match Best Local Similarity Matches 25; Conserva

A;Reference number: Z19031 A;Accession: T18856

A,Reference number: 219917 A,Accession: T24653

Ouery Match Best Local Similarity 30.8% Matches 24; Conservative

A.Gene: CESP:C02B4.1

A: Map position: X

A,Molecule type: mRNA A,Residues: 1-610 <MAS> A,Cross-references: DDBJ:AB042840

A,Accession: PC7105 A.Accession: JC7530

Special human popilionavirue type 53 Concean human popilionavirue type 53 Concean human popilionavirue type 53 Concean human popilionavirue type 53 Concean human popilionavirue type 53 Concean human popilionavirue type 53 Appendix human popilionavirue types 54 Appendix human popilionavirue types 54 Appendix human popilionavirue types 54 Appendix human popilionavirue types 54 Appendix human popilionavirue types 54 Appendix human popilionavirue types 54 Appendix human popilionavirue types 54 Appendix human popilionavirue types 54 Appendix human popilionavirue types 55 Appendix human pop	RESULT 14 SMEANT 14 OBST 70 process. To proceed the process of t	Approprietation in Emphasized to Minglasop profession in Digitals and Minglasop and Mi	Outry March Bone Local Similarity 13-89; Pred. No. 49: Matches 25; Conservative P. Mismarches 12; Indels 9; Gape 3;	Cy 1_LYSURGERYPERMANCETRARIA-LANGUAGHTED-ESCRILAVALD 56 Db 11_LIII.surgery.evAcorrept-principles reputation to 110 Db 110 dAAMSTOCKER 141 Db 110 dAAMSTOCKER 141	BBSUZ 15 SAUTO RELICOPOSESSAR [EC 3.4.24) H-II precureor - carpet wiper (fragment) N'consains: distincegrin
Necessary 12 Conservatives 3; Westerbee 31; Finds 13; Gaps 4; Michael 22 Conservatives 3; Westerbee 31; Gaps 4; Organization 22 Conservatives 3; Westerbee 31; Gaps 4; Conservatives 32 Conservatives 3; Westerbee 31; Gaps 4; MARCHAEL 32 CONSERVATIVE 3; Westerbee 32; Gaps 32; Gaps 33; Gaps 33; Gaps 33; Gaps 34; Gaps	Owny Watch 16.3%; Score 66; DB 2; Inegch 826; Swell Look Bantharty 55.3%; Peeblo 56; 27; Indele 34; Gaps 5; Naches 35; Conservative 11; Mistaches 277; Indele 34; Gaps 5; Oy 9: PICPUNISP	Nation 12 Nation	A.Nocheus proliminary A.Nocheule (1991 UNA A.Nocheule (1992 UNA A.Nocheule (1993 UNA A.NOCHEUL) A.Nocheule (1993 UNA A.NOCHEUL) A.Nocheule (1993 UNA A.NOCHEUL) A.Nocheule (1993 UNA A.NOCHEUL) A.Nocheule (1993 UNA A.NOCHEUL)	Competies: Management of the competition of the com	Oy 9 SQUARREREALANDARABLEMOCROPERPOLEGAGESTALMENDER 59 Db 304 RESCRAMORPELALGANIAASISDOWARMONTRENDESCOLOMIFLIPOIPE 355 E

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C Species; 16-Der-1956 Senquence_ravison 0c-Der-1956 Front_change 09-Jun-1000
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Query Match
16.0%; Score 64; DB 2; Length 549;
Set Local Sainlarity 27.2%; Pred. No. 19;
Matches 25; Conservative 8; Wismatches 23; Indels 36; Gaps

46 SCSRLLVPLLD-----GTECGVEKWCSKGRC 71

514 MCR---YPYGDEGWYDPGTXCEDXXVCINGKC 542

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Search completed: March 13, 2004, 07:44:36 Job time : 3.4776 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence: Searched:

1 PGLYYSANEQCRVAFGPKAV......VPLLDGTECGVEKWCSKGRC 71

Total number of hits satisfying chosen parameters: 141681 seqs, 52070155 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is detrived by analysis of the cotal score distribution. SwissProt_42:*

SUMMARIES

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Q9ukp5 homo sapien	Q05910 mus musculu	Q87qx6 vibrio para	P36797 human papil	Q05284 mycobacteri	P82942 naja kaouth	O13766 schizosacch	Q60411 cavia porce	Q13443 homo sapien	Q9z319 mus musculu	P07357 homo sapien	P59222 mus musculu	
ATS6 HUMAN	AD08 MOUSE	GLC1_VIBPA	VE2 HPV53	VG70 BPML5	KAOU NAJKA	YE94 SCHPO	AD02_CAVPO	AD09 HUMAN	CORI_MOUSE	CO8A HUMAN	SRC2_MOUSE	
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66.5	99	65.5	65	64.5	63	63	62	62	62	61	61	
34	35	36	37	38	39	40	41	45	43	44	45	

ALIGNMENTS

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15.4MA-2004 (BL. 43. Late monostion update)

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SPACES.
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TSP TYPE-1 3.
TSP TYPE-1 4.
TSP TYPE-1 5.
FLAC.
CYSTERNE SWITCH (POTENTIAL).
ZINC (CATALATIC) (SF SIMILALITY).

BY SIMILARITY. ADANTS-19. METALLOPROTEASE. DISINTEGRIN-LIKE.

TSP TYPE-1 1. CYS-RICH.

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BY SIMILARITY. ADAMTS-3. PROPER DOMAIN CHAIN

METALLOPROTEASE. DISINTEGRIN-LIKE. TSP TYPE-1 2. TSP TYPE-1 3. TSP TYPE-1 4. TSP TYPE-1 1. CYS-RICH. SPACER 250 DOMAIN NIAMOC DOMAIN DOMAIN DOMAIN

macrix (By sintarty).

- 1150NB SECFICITY: Found in cartilloge and skin.

- 1- DOWNIN: The spacer demain and the TSP type-1 domains are important for a tight interaction with the extracellilar material.

- 1- PTW. The Speciment is Cleaved by a furn endopspilates (By - PTW. The Speciment is Cleaved by a furn endopspilates (By -Windlings of the properties of similarity Relongs to peptidase family M128.
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SMILARITY Contains 1 PLMC domain.
SMILARITY Contains 1 PLMC domain.
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18-FSB-2003 (Rel. 4), Created)
18-FSB-2003 (Rel. 4), Last sequence update)
18-FSB-2004 (Rel. 4), Last amocation update)
18-MAR-2004 (Rel. 4), Last amocation update)
18-MAR-2009 (Rel. 4), Last amocation update)
18-MAR-2009 (Rel. 4), Last amocation update) AT12 HUMAN P58397; T 5 HUMAN

472 PGINYSMDEQCREDFGVGYKMCTAPRT-FÖPCKQLWC-SHPDNPYFCKTKKGPPLDGTEC 529

à

RESULT

1 PGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC

(1997) (1

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ACT SITE METAL

RINI GTAL

(BY SIMILARITY)

ZINC (CATALYTIC) BY SIMILARITY. PLAC. POLY-ARG.

09

Gaps

5

Length 1205; 32; Indels

Score 144, DB 1, Pred. No. 1.2e-08; 5; Mismatches 32;

36.1%;

Local Similarity 45.1%; see 32; Conservative

Best Loc Matches

Homo sepiens (Human), Bakaryote, Metasoa, Chordata, Craniata, Vertebrata, Buteleostomi, Memalia, Butelberia, Primates/ Catarthini, Hominidae; Momo. NCBL Textbefots,

indigenome TOMO NA. A STATEMENT TO STATEMENT

origin. The spacer domain and the TSP type-1 domains are important for a tight interaction with the extracellular matrix (By

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--- SIMILARITY: Belongs to peptidase family M128.
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--- SIMILARITY: Contains 8 758 type-1 domains.

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the European Bicinformatics Institute. There are no restrictions on its	way	cial	'eou	
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1 PGLYYVYHQQQQLQYGSNA---FQCEVAVVQQTLMGSV----KGEVGSKLDAAADQTQC S20

521 GEKKWCMAGKC 531

61 GVERWCSKGRC 71

8 8

CFC-2003 [Rel. 42. Created by Careton Under 10. CFC-2003 [Rel. 42. Last sequence update) 10-CFC-2003 [Rel. 42. Last semocation update) 10-CFC-2003 [Rel. 42. Last semocation update) with Windows CFC 2-Last 4. (A distinguish and metalloproteinase with thromologoudin motifs 18 (40,04-75 18) [ADMA-7518).

PRT; 1081 AA

STANDARD;

AT18 HUMAN

Homo sapiens (Human). Bukaryoda, Metazos; Chordats; Craniats; Vertebrats; Euteleostomi;, Mmmmalia, Eutentis; Primates; Cstarthini; Hominidae; Homo. NCBL TaxID=9606;

ADAMTS18.

license agreement (See nttp://www.isb-sib.cn/annor	. (11)			Disintegrin.	A ZD BS	Jase Mi2B.	fase_M128_N.		open, 1,	i i		ri.		FAI	ALSE NEG.	ALSE			, Zinc, Signal, Glycoprotein, Zymogen,	POTENTIAL.	BY SIMILARITY.	S-12.	METALLOPROTEASE.	н	Cvs.bich	SPACER 1.	TSP TYPE-1 2.	TSP TYPE-1 3.				TSP TYPE-1 7.	YPB-1	PLAC.	POLY-GLU.	CTTVIET	į	_	ALYTIC) (BY SIM	(GLCNAC)		GLCNAC	(GLCNAC)	?	(GLCNAC)	N-LINKED (GLCNAC) (POTENTIAL) .	GLCRAC	(GLCNAC.	(GLCNAC)	-	N-LINKED (GLCNAC)	on; createseasta cac
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or send an email		EMBL, AJ2	MIM, 606184;	InterPro,	InterPro	InterPro,	InterPro,	InterPro;	Pfam: PF0:	Pfam, PF0	Pfam; PF0	PRINTS, P	DECKT SM	PROSITE,	PROSITE,	PROSITE;	PROSITE,	PROSITE,	Hydrolase	STGNAT.	PROPER	CHAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOKAIN	DOMAIN	DOMAIN	DOMAIN	DOMETIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	METAT	ACT SITE	METAL	METAL	CARBOHYD	CARBORIO	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARROHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	
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or send an email to licensesisb-sib.ch)
EMBL: AJ311903; CAC83612.1; -.

Sydrolage, Metalloproteage, Zinc, Signal, Glycoprotein, Zymogen,

7; Gaps

36.0%; Score 143.5; DB 1; Length 1593; 38.0%; Pred, No. 1.98-0B; 1.08 12; Mismatches 25; Indels 7;

Ouery Match Best Local Similarity 38.01 Matches 27; Conservative

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	9	NKED (GLCNAC) (POT NKED (Score 135, DB 1, Pred. No. 1.3e-07; Mismatches 32; ACTPAREHLDMCQALSCHT
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76 PGLHYSMNEQCRFDFGLGYMMCTAFRT-FDPCKQLWC-SHPDNPYFCKTKKGPPLDGTWC 533

61 GVERWCSKGRC 71

534 APGKHCFKGHC 544

RESULT

Fidelity of 1861, 40, the sequence update)

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Bikaryota; Mataroa; Chordata; Craniata; Vertebrata; Buteleoscomí; mamalia; Butheria; Primatos; Catarthini; Hominidae; Homo. NCBI_Tax10-9606; fomo sapiens (Human)

SEQUENCE FROM N.A. (ISOFORMS LPNPI AND SPNPI), AND DISEASE

matrix (By similarity). ALTERNATIVE PRODUCTS

Svent-Alternative splicing; Named isoforms=2; Name=LpNPI, IsoId=095450-1; Sequence=Displayed;

This strict story marry is copyright. It is produced through a collaboration between the Suisa institute of Bioinformation and the RBEL outration. The Runpass in Onlinearise Institute. There are no restrictions on its Many and Profit is machinitations at long and an opposite and profit is machinitation at long and an opposite and an example of the Research of the INCLOSES. SEQUENCES DESIGNATIONS DESIGNATION OF SEQUENCES DE SEQUENCES F. Editors Defects and Annual and an ensee of these nonless of these houses by you will feet with the state of the state o PROSTITE PROSTITE PROPERTY PALES NO.
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Bukaryota, Metazoa: Chordata, Craniata, Vertebrata, Buteleostomi, Mommalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinse, Mus. McCall'Asid-10090.

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SEQUENCE FROM N.A. (ISOPORM A).

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BOLZ H., Semirez A., von Brederlow B., Kubisch C.,

"Characterization of ADMYS14, a novel member of the ADAMTS

metalloproteinase family.", Brochim. Biophys. Acta 1522:221-225(2001).

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IsoId=08MXS8-3; Sequence=VSP_006958, VSP_005501; Note=Produced by alternative_splicing of isoform B; IsoId=08WXS8-2; Sequence=VSP_006958;

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EMBL, AF358666, AAL40229.1; -. EMBL, AJ345098, CAC87943.1; -. EMBL, AF366351, AAL79814.1; -. MERCPS, M12.024; -. Genew; HGNC:14899; ADAMTS14. (IM) 607506;

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                                    75 1427 VON WILLEBRAND FACTOR-CLEAVING PROTEASE. 1427 AA; 153632 MM; EBIBCSAABCIA4442 CRC64;
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Mammāla, Buhheria, Rodentia, Sciurognathi, Muridae, Murinae, Mos
NGE, Taxile-10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa Chordata; Craniata; Vertebrata; Buteleostomi; Nommalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. "Ariba ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 1966) ("Ariba 196
                                                                                                                                                                                                 y Match 100.04, Score 399, DB 4; Length 1477; Local Similarity 100.04; Pred. To. 16-43, D. 16-48; Local Sinitarity No.04; Pred. To. 16-43; O. Indels O. Mismarches O; Indels O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.7%; Score 242; DB 4; Length 364;
97.7%; Pred. No. 1.5e-23;
tive 1; Mismatches 0; Indels
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01-448-2003 (TEMBER-21. 23, Last sequence update)
01-007-2003 (TEMBER-21. 25, Last ambitation update)
ADAMPS-12 precursor (Fragment).
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STRAIN=CS7BL/6J; TISSUB=Head;
MEDLINE=22354683; PubMed=12466851;
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THEEPPO, IPR000085; TSP1.
FABNIS, PR001705; TSP2.
SWART, SW00705; TSP1.
PROSITE, PS00022, TSP1.
1.
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Best Local Similarity 97.7%
Matches 42, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GVEKWCSKGRC 71
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Charleton V., Bong L., Aghayami A., Corleon V.;
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Change M., Chaves C., Orgente V., Charlette D., Friese E.,
Change M., Monsai C., Charlette M., Sandalla E., Barges W., Landa M.,
Recomparation M., Monsai C., Man M., Yu C., Arais S. E., Rubin O.M.,
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Physics N. Empirod. 778 (2015)

Olymonic Manual M. (2015)

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                                                                                                                                              Mus muscullus (Mouse).
Shikayoosa Shikazoosa Chardata, Cranista, Vertebreta, Shielaosionli, Mammilai, Shicharia, Rodentia, Sciurognathi; Muridae, Murinae, Mus. Musl. FaxID=10090;
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33.6%, Score 134, DB 11; Length 1092;
Best Local Similarity 36.6%, Pred. No. 99-09, No. 89-09, Maches 26; Conservative 11; Missarches 30; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COSSI ON DEDNA GOMESS.
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08450-091-004-2002 (TEMSLTE1. 21, Created)
01-004-2002 (TEMSLTE1. 21, Last sequence update)
01-007-2003 (TEMSLTE1. 25, Last annocation update)
01-MAR-2003 (TrEMBLrel, 23, Last sequence update)
01-Oct-2003 (TreMBLrel, 25, Last annotation update)
Mypothetical metalloprotesse.
E130314N14RIX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE PROM N.A.
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472 PGVIYDVHHQCQLQYGPNA---TFCQEVENVCQTLMCSV----KGFCRSKLDAAADGTRC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          506 PGOLYDANTOCKWOFGERAKLCMLDFRK---DICKALWCHR---IGRKCETKFMPAAEGT 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery March

14.3%; Score 137; DB 11; Length 900;

Best Local Shillarity 19.1%; Pred. No. 2.9%-0.89; Indels 8; Gaps

Machens 23; Conservative 8; Mismatches 28; Indels 8; Gaps
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                                                                                                                                                                                                                                                                                                                                    Owery March 15.5%, Score 141.5, DB 11, Length 1600, Beet Local Stailarity 300% Peed No. 113-0.9, Indels 7; Gaps Marches 26, Indels 7; Gaps
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Mommadias Eucherica, Rodentias, Sciurognachii, Muridae, Murinae; Mus. 
(NET_raxID=10090);
                                                                                                                                                                                                Integrin, Protease. -
SEQUENCE 1600 AA; 17791 MW; 083089D356E38C5D CRC64;
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SEQUENCE 900 AA, 100679 MW, 590BE2B0B73740FF CRC64,
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01-0CT-2002 (TransLel. 22, Last sequence update)
10-0CT-2003 (TransLel. 23, Last annotation update)
10-0CT-2003 (TransLel. 23, Last annotation update)
10-0CT-2003 (TransLel. 23, Last
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01-MAR-2003 (TrEMBLrel. 23, Created)
                                        PROSITE; PSS0215; ADAM MRPRO, 1.
PROSITE; PSS0092; TSP1; 6.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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          SMART; SM00209; TSP1; 8.
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Gaps

1 PGLYYSANBOCRVAFGEKAVACTFAREHLDWCQALSCHIDPLDQSSCSRLLVPLLDGTEC 60 215 PGERFNANOCHLRPGKNFMQAS-TQSKMEICRDLHCRODGLPWTS-----HPALEGTEC 268 Without Control No. 1 Acrison B No. 1 Acrison A Meanwright of Many Carlot and Market and M Williams S., Woodeg T., Worlty K.C., Wh. D., Wang S., Ywo G.A., Yes J., Who R.F., Zaveri J.S., Zhan M., Zhang G., Zhao G., Zheng L., Zheng Y., Zhong S., Zhong K., Zhong W., Zhou K., Zhu S., Smith H.O., Gibbe B.A., Wyers E.W., Rhinn G.W., Ventre J.C., Zhu K., Smith H.O., The genome agenome of Crosophila welanogester.'' Drosophila metanogaster (Fruit fly). Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, 31.6%; Score 126; DB 5; Length 790; 35.2%; Pred. No. 7.2e-08; 1.4ve 13; Mismatches 27; Indels Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Přam: PPO(42): Reprolymin: 1. PROSTIE: PSSO12: ADM/ARPNO; 1. PROSTIE: PSSO12: TSP1; 1. PROSTIE: PSO14: ZINC. PROTES: 1. GMP125 PRELATION (TERRETE 13, Created) O1-5AY-2000 (TERRETE 13, Last sequence update) Conservative 269 GPNWWCRGGTC 279 01-XAY-2000 (TERMELTE). 01-OCT-2003 (TERMELTE). CG3622 protein. CG3622 OR BCDNA:GM08694. 61 GVBKWCSKGRC 71 Query Match Best Local Similarity Matches 25, Conservat SEQUENCE FROM N.A. SEQUENCE PROM N.A. RESULT 9 9ZTM6C ò 24444888888 215 PGERFNANGCMLRFGKNFWQAS-TQSKMEICRDLHCRQDGLPWTS----HPALEGTEC 268 09 1 PGLYYSANEGCRVAFGPXAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC Gaps Drosophila melanogaster (Fruit fly). Bristychs, Wetsora, Arthropoda; Hakspoda; Insecta; Plerygota; Noptera; Endoperygota, Diptera; Brachycera; Maccomorpha; Ephydroidea; Drosophiladae, Drosophila. Length 790; 25; Conservative 13; Mismatches 27; Indels 01-OCT-2002 (TEMBLE). 22 Created)
01-OCT-2002 (TEMBLE). 22, Last sequence update)
01-OCT-2003 (TEMBLE). 25, Last annocation update) Query Match 31.6%; Score 126; DB 5; Best Local Similarity 35.2%; Pred. No. 7.2e-08; 269 GPNWCRGGTC 279 PRELIMINARY; CG3622 OR BCDNA:GM08694. 61 GVEKWCSKGRC 71 SEQUENCE PROM N.A. NCBI TaXID=7227; STRAIN-Berkeley; OBMME1 RESULT 8 DBMMEL 85555555

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6; Gaps

Wilshings Trough M. Hammoon N., Maraumoto M., Ja Wilshings Trough M. Hammoon N., Maraumoto M., Ja Wallings M. Hammoon M., Maraumoto M., Ja Wallings M. Hammoon M., Maraumoto M., Ja Wallings W., Ja Wallings W

"Genome sequence of the nematode C.elegans: A platform for givestigating bloopy.";
Sizence 283:2012-2018 [1998]

88444448

Lennard N.; Submitted (JUN-1996) to the BMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A. MEDLINE=99069613; PubMed=9851916;

CONTROL OF CONTROL OF

509 A.A. PRT;

PRELIMINARY;

	1 POLYTRANDICAN, PRINTANA,	PRAVACTEAREH PERVACTEAREH PERC 71 C 73 C 459 RRT;	IOYFHEQS	ONCGALSC 	HTDPLD
388	GELUKITROCOVARIO LEGIBECGVERMCERG	PTEIPCLH	IGYFHBQS	SICERIMO	SDGESD
4	LDGTBCGVBRWCBKG 	459 PRT;	269 AA.		
	PRELIMINARY,	459 PRT;	269 AA.		
ESULT 11		PRT;	269 AA.		
acros.		PRT;	269 AA.		
D 09GL54					
C 09GL54:					
T 01-MAR-2001					
	(TrEMBLrel.		ence upd	date)	
DT 01-0CT-2003	3 (TrEMBLrel. 2	Last annotation update	tation u	update)	
	Aggrecanase-2 (Fragment).				
	Orvetolagus cuniculus (Rabbit).	bbit).			
oc Bukarvota;	Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,	ata, Craniat	a; Verte	sbrata;	Butele
_	Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus	orpha; Lepor	idae; or	ryctolas	n8.
OX NCBI_TaxID=9986;	i=9986;				
	ROM N.A.				
RA Goad D.L.,	Goad D.L., Goad M.E.,				
	"Molecular cloning of labine accrecanase-2 (ADANTS-11) from artic	ine addrecan	ase-2 (2	ADAMTS - 1	(1) fro

RESULT 10 020930

cular

1-1VP 53 NYFP 441 Saps

31.2%; Score 124.5; DB 5; Length 509; 34.6%; Pred: No. 7.2e-08;

Query Match Best Local Similarity

4, Gaps

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1 PGLYYSANEÇCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 PGGTYDATQQCNLTFGPEYSVC----PGMDVCARLMCAVVRQ3GNVCLTXXLPAVEGTPC 235
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Agracianies ("Persona")
Bloarycta, Westson ("Creal, Crealists, Vertebrats, Bucaleostoni,
Richarycta, Westson ("Creal, Crealists, Vertebrats, Bucaleostoni,
Ness, Taxibashis Personalists Buches, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bquides, Bq
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                                                                                                                                                       30.3%; Score 121; DB 6; Length 187;
33.8%; Pred. No. 7.38-08;
tive 11; Mismatches 32; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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4; Gaps

RESULT 13 (1989) 11 (1989) 11 (1989) 12 (1989) 13 (1989)

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478 PGTSYDANRQCQFTFGEDSKHCPDA---ASTCSTLWCTGTSGGVLVCQTKHFPWADGTSC 534
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                                                                                                                   Bikaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
(MSE_TaxIn-9666;
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Memedia: Butheria: Perissodacty Craniata: Vertebrata; Buteleostomi;
Memedia: Butheria: Perissodactyla: Equides; Equus.
VESL_TAXLD9789;
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29.9%; Score 119.5; DB 4; Length 967;
Best Local Similarity 36.6%; Pred. No. 6.5e-07.

Matches 26; Conservative 3; Mismatches 39; Indels 3;
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01-MAR-2003 (TrENBLrel. 23, Last sequence update)
01-OCT-2003 (TrENBLrel. 25, Last annotation update)
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Human von Willebrand factor (vWF) -cleaving enzyme-related protein (first entry) 5-MAY-2003 AA016618;

Human; protease inhibitor; gene therapy; vWF-cleaving enzyme; von Millebrand festor-cleaving enzyme; thrombocycopenic purpura; wyocardial infarction; oreebzal infarction; arreriosolerosis; placelet thrombosis; etenosis.

Homo sapiens

WO200288366-A1 07-NOV-2002 25-APR-2002; 2002WO-JP004141

25-APR-2001, 2001JP-00128342. 27-JJL-2001; 2001JP-00227510. 28-SRP-2001; 2001JP-00302977. 25-JAN-2002; 2002JP-0001596.

Hamamoto T, Nakagaki T; Maeda H, Nozaki C, KAGA) CHEMO-SERO-THERAPEUTIC RES INST Mimura N, Soejima X,

von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and applicable in diagnosis of, and applicable in diagnosis of himeabotic himeabotic himeabotic himeabotic diagnosis of exploration and occebral infarction and occebral infarction. WPI; 2003-120479/11. N-PSDB; ABT32584.

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Claim 4; Page 92-101; 144pp; Japanese

Willebrand factor (VWF) - cleaving enzyme-related protein Sequence 1297 AA;

Gaps 0 Length 1297; Indels . Score 399; DB 6; Pred. No. 2.9e-40; 0; Mismatches 0; Local Similarity 100.0%; los 71, Conservative 0

AAE24449 standard; protein; 1353 AA RESULT 3

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Gaps

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Human Von Willebrand factor-cleaving protease fragment #2 (first entry)

04-OCT-2002

AAE24449;

Human, Von Willebrand factor-cleaving processe; VVP-cp: therspy, enzyme: througenic anisable, immunisable, i

20-NOV-2001; 2001WO-SP013391. 30-MAY-2002

10200242441-A2

domo sapiens

Furlan M, Turecek Kerschbaumer R, 22-NOV-2000; 2000US-00721254. 12-APR-2001; 2001US-00833328. Laemmle B, Gerritsen HE, F. Scheiflinger F, Antoine G, Zimmermann K, Voelkel D; (BAXT) BAXTER AG

P, Schwarz H; Tagliavacca L;

Novel isolated or substantially purified von Willebrand factor-cleaving processe, useful for producing preparation for therapy of thromboes and thromboemolic disease such as thrombotic thromboeving purpura. WPI; 2002-479950/51

Claim 1, Page 64-68; 93pp; English.

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                                                                                                                                          61 GVERWCSKGRC 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 PGLYYSANECCRVAPGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 286
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pagabementary therapy for, thromboch chrombochyopmic pupus, and for
developing drugs for e.g. myocardial infarction and cerebral infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                               Score 399, DB 5; Length 1353;
Pred. No. 3e-40;
0; Mismatches 0; Indels 0;
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Maeda H, Nozaki C,

Soelima K, Mimura N, WPI; 2003-120479/11.

N-PSDB: ABT32583.

Claim 4; Page 82-92; 144pp; Japanese.

Sequence 1353 AA;

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(KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

25-APR-2002; 2002W0-JP004141. 25-APR-2001; 2001JP-00128342. 27-JUL-2001; 2001JP-00227510 28-SEP-2001; 2001JP-00302977 25-JAN-2002; 2002JP-00017596

AA016617 standard; protein; 1353 AA

AA01661 RESULT

(first entry)

15-MAY-2003

AA016617,

platelet thrombosis; stenosis,

WO200288366-A1. Homo sapiens.

37-NOV-2002

100.04,

71; Conservative

Similarity

Query Match Best Local fragment

Sequence 1353 AA;

888

Claim 4; Fig 2; 31pp; English.

61 GVEKWCSKGRC 71

RESULT 6

04-OCT-2002 (first entry)

Human Von Willebrand factor-cleaving protease (vWF-cp).

52. .1427 224. .228 Cleavage-site Home sapiens Peptide Protein Region Region 11111111111111111

note= "Catalytical side" 'note= "Met turn"

301. .377 /note= "Distintegrin like motif"

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Gaps 0 Omery March 100.0%; Score 399; DB 5; Length 1415; Best Local Similarity 100.0%; Pred. No. 3.2e-60; Matches 71; Conservative 0; Masanches 0; Indels 0; Sequence 1416 AA,

384 GVEKWCSKGRC 394

AAB24450 standard; protein; 1427 AA.

Human; Von Willebrand factor-cleaving proteases vWF-cp; therapy; enzyme; transgenie namia. Immuniatelion introdecaholic disease; preeclampsis, transgenie almia. Thromboorpic prepurs; TTP; Memoch-Schonlain purpurs; TTP; Memoch-Schonlain purpurs; transgenies; mencals incomboorpic purpurs; TTR; transgenies; mittoospilan; chromboore 8;

/note= "Mature human vMF-cp protein" 69. 75 /note= "Furin cleavage site" label= Signal peptide Location/Qualifiers

nomain

187. .439 /note= "Thromspondin type I motif" note= "Spacer" 888. 743 'note= "Thromspondin type I motif" note= "Cysteine rich region" .553 .687 802 Domain Domain Region Region Domain

18-03-00 / 12 2 COPY 32-4

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'note= "Thromspondin type I motif" 997. .952 /note= "Thromspondin type I motif" /note= "Thromspondin type I motif" /note= "Thromspondin type I motif" .1013 Domain Domain Domain

Domain

note= "Thromspondin type I motif"

WO200242441-A2.

20-NOV-2001, 2001WO-EP013391 30-MAY-2002

22-NOV-2000; 2000US-00721254. 12-APR-2001; 2001US-0083328.

Lagemile B, Gerritsen HE, Furlan M, Turscek P, Schwarz H; Scheiffliger F, Antoine G, Kerschbaumer R, Tagliavacca L; Signemennen, Woelkel D; BAXT | BAXTER AG.

WPI, 2002-479950/51. N-PSDB; AAD39332.

Novel isolated or substantially purified Von Willebrand factor-cleaving procease, useful for producing preparation for Thorapy of thrombosis and biromboseolic disease such as thrombotic thrombovysts purpura.

Claim 1, Fig 5, 93pp; English.

The invention process (VMF cp) polyperide. WF-cp is useful for the invention process (VMF cp) polyperide. WF-cp is useful for the interface of

Sequence 1427 AA;

100.0%; Score 399; DB 5; Length 1427; 100.0%; Pred. No. 3.2e-40; tive 0; Mismatches 0; Indels 0; Query Match Best Local Similarity 100.0 Matches 71, Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1 (a); Page 154-157; 200pp; English.
ABB98125 Standard; protein; 1445 AA
                                                                                                                                                                                                                                        Human PMSM Incyte ID 7473607CD1.
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21-DEC-2000; 2000US-0557803P.
05-XAN-2001; 2001US-026010P.
19-XAN-2001; 2001US-0262851P.
25-JAN-2001; 2001US-0264623P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-2001; 2001WO-US046964.
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                                                                                                                                                             .7-OCT-2002 (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABQ75946.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fomo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUN-2002.
                                                                                  ABB98125;
                                         The investigate and states to a wood hand appearance propriet and the box exequence which encodes it. Agreem is a short extrediblish and the box expendible for providing a controller extraction and the proposition of an extraction and the providing and the propression of another and the providing and an extraction and an expendible for the canner of another and an expendible for the canner of another and an expendible for the canner of another and an expendible for the canner of another and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension and an expension are proposed as an expension as a property and an expension and an expension are proposed as a property and an expension and an expension are property and an expension and an expension are property.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 POLYYSANEGCRVAPGPKAVACTPAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 60
                                                                                                                                                                                                                                                                                                          aggiecanase, aggiecan, articular cartilage, proteoglycan proteolytic, 
training department of trammcory) form disease; 
antarthifus, opeoppathor antiinfhamacory; 
antarthifus, opeoppathor antiinfhamacory; 
professimes—asociated disorder; opeoarthifis; inflammatory condition; 
human, enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 399, DB 7; Length 1427;
100.0%; Pred. No. 3.2e-40;
iive 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolared DNA molecule encoding an aggrecanase polygaptide for 
producing a purified human aggreconase protein which can be used to 
develop inhibitors of aggrecanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Racie LA, Twine NC, Agostino MJ, Wolfman N, Morris EA;
                                                                                                                                                                                                                                                        Human aggrecanase protein amino acid seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; SEQ ID NO 8; 24pp; English.
        ADD94038 standard; protein; 1427 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMHP : AMERICAN HOME PROD CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 JAN-2002, 2002US-00057487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001, 2001US-00978979.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GVEKWCSKGRC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 2003-801251/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB, ADD94037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003105313-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                     29-JAN-2004
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                                                                                           ADD94038,
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ADD94038

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mamunosuppensivo, anti-tify datisfabancio matiraterologistico, ALDS;
hypotensivo, gene horany, catdionopathy, atheroacenosis hypertension of coopenial bart defect; notice menosis arrial sepola defect; notice menosis arrial sepola defect; notice manuscribular onal defect; pulmonary senosis prostate cancer; userino encer; pratir veneral bent disease; militable accessis profice qualitate control profit arthus, oquired immunodeficiency syndrome; (cohmic disease, brocchial anthus).
                                                                                                                             304 PGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 363
                                                                                                       1 PGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 60
                                                                                                                                                                                                                                                                                                                                                            Human; NOVX; G protein-coupled receptor; cytostatic; cardiovascular;
found to have homology with B. taurus procollagen I N-proteinase
                                                                            0
                                                   Length 1445;
                                                                            Indels
                                                 ; Score 399; DB 5;
; Pred. No. 3.2e-40;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome mapping, forensic identification.
                                                                                                                                                                                                                                                     ABR96171 standard; protein; 984 AA
                                                                                                                                                                                                                                                                                                                                    Human NOV17a protein SEQ ID NO:84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-0289817P.
2001US-0289818P.
2001US-0290194P.
2001US-0290753P.
                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-0289620P.
2001US-0289620P.
2001US-0289621P.
                                                                                                                                                                                                                                                                                                        15-8EP-2003 (first entry)
                                                                              71; Conservative
                                                                                                                                                                                 364 GVEKWCSKGRC 374
                                                                                                                                                           61 GVEKNCSKGRC 71
                                                 Query Match
Best Local Similarity
                        Sequence 1445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W0200290568-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-2001;
08-MAY-2001;
09-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-2001;
14-MAY-2001;
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                                                                                                                                                                                                                                          ABR96171
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87.3%; Score 348.5; DB 6; Length 984; 90.1%; Pred; No. 3.8e-34;
                                    0; Indels
                                        0; Mismatches
                      Local Similarity 90.1%;
les 64; Conservative (
       Query Match
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Sequence 984 AA;

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New NOVY polypeptides and polymeterides useful for treating or more actions and action to the more action to the more action to the more defenced and the confidence of the more defenced and the confidence and the more action that of the more actions and actions and actions and actions are actions as a second actions and actions are actions as a second action and actions are actions as a second action and actions are actions as a second action and actions are actions as a second action and actions are actions as a second action and actions are actions as a second action and actions are actions as a second action action actions are actions as a second action action actions are actions as a second action action actions are actions as a second action action actions are actions as a second action action actions are actions as a second action action actions are actions as a second action action actions are actions as a second action action action action actions are actions as a second action ac

WPI: 2003-111987/10.

N-PSDB; ACF16980.

Claim 1; Page 173; 491pp; English.

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Gaps

CURA-) CURAGEN CORP

513 PGLYYSANEQCRVAFGPRAVAC------DWCDALSCHIDPLDQSSCSRLLVPILLDGTEC 565 1 PGLYYSANEQCRVAPGPKAVACTFAREHLDWCQALSCHTDPLDQSSCSRLLVPLLDGTEC 60 61 GVEKWCSKGRC 71 g ò

AAG63829 standard; protein; 1120 AA RESULT 10

S66 GVBKWCSKGRC 576

29-OCT-2001 (first entry)

2001US-0293747P. 2001US-0294434P. 2001US-0312192P. 2001US-0313173P. 2001US-0313187P. 2001US-0318728P. 2001US-0333891P. 2001US-0333942P. 2002US-0345776P. 2002US-0345220P. 2002US-00136071.

24-MAY-2001; 25-MAY-2001; 29-MAY-2001;

MAY-2001; MAY-2001; 30-MAY-2001; 14-AUG-2001; 17-AUG-2001;

2001US-0318744P.

12-SEP-2001; 15-NOV-2001; 28-NOV-2001; 28-NOV-2001;

03-JAN-2002; 04-JAN-2002; 01-MAY-2002;

2001US-0291189P. 2001US-0291243P. 2001US-0292001P. 2001US-0292587P. 2001US-0293107P 2001US-0293589P.

15-MAY-2001; 18-MAY-2001; 21-MAY-2001;

The state of the s Amino acid sequence of a human zdint5 polypeptide.

'note= "potential N-linked glycosylation site" notes "potential N-linked glycosylation site" notes "potential N-linked glycosylation site" note- "potential N-linked qlycosylation site" 'note= "potential N-linked glycosylation site"

note: "unspecified residue encoded

"Dotential N-linked qlycosylation site"

noten

note= "potential N-linked glycosylation site"

Jocation/Qualifiers

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New anti-angiogenic intestinal polypoptides zdint5 polypoptides, which are methers of distincting in proceases, for modulating extracellular matrix interaction, tunor suppression and wound healing.
                                                                                                                                                                                                                      Claim 2, Page 84-88; 92pp; English.
                                                                                                                                   09-FEB-2001; 2001WO-US004198
                                                                                                                                              0-FEB-2000; 2000US-00501806.
                                                                                                                                                                    Holloway JL, Sheppard PO,
                                                                                                                                                         ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                WPI, 2001-522477/57.
                                                                                                                                                                                      N-PSDB; AAH74765.
                                                                                                             40200159112-A1
                                                                                                                        16-AUG-2001
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The properties of the properti The zdint5 The present sequence represents a human zdint5 polypeptide.

Sequence 1120 AA

28 Gaps 12: 64.2%; Score 256; DB 4; Length 1120; 72.0%; Pred, No. 1.3e-22; ive 0; Mismatches 9; Indels 12 Conservative Ouery Match Best Local Similarity **Ase 54; Conserva

331 GLYYSANEQCHVAFGPPG----CRLHLRQGAPCQALSCHIDDQSSCSRLLVPLLDGT 385 2 GLYYSANEQCRVAFGFKAVACTFAREHLDM---CQALSCHTDFLDQSSCSRLLVPLLDGT

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ECGVEK ---- WCSKG 69 69

386 ECGVEKVHGRWSSWG 400

RESULT 11

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zdints; ADAM; a disintegrin and metalloprotease, detergent;
                      ABG74113 standard, protein; 1120 AA
                                                                                                                               01-MAY-2003 (first entry)
                                                                                                                                                                                            duman mature zdints
                                                                             ABG74113;
ABG74113
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Thrombospondin domain.

Home sapiens

note= "Encoded by TIN" Location/Qualifiers label UNKNOWN Misc-difference 474

1118. 1119 /note= "Encoded by CTGTGAAAT" Misc-difference US2002142439-A1

99-FEB-2001; 2001US-00781080 .0-FEB-2000; 2000US-0181511P

(HOLL/) HOLLOWAY J L. (SHEP/) SHEPPARD P O. (YAMA/) YAMAMOTO G.

Yamamoto G, Holloway JL. Sheppard PO,

N-PSDB: ABX15947, ABX15948. (PI) 2003-174136/17

New zdint5 polypoptides, useful for diagnosing, preventing or treating rumor formation, Crohn's disease, inflammatory bowed disease, food poliening, melanoma, degenerative disease, batterial infection, or for wound healing

Claim 2; Page 32-34; 37pp; English.

The mirements or states to an assisted polypoids, statists, of distincents and metalloprocease [AMM], the gues for which is located on human formerness [94], a comprising the metalloprocease death. Interdepondant (Commisses [94]) and starte process. In the statistic process, in the statistic process of the statistic process. In the statistic process of the statistic process of the statistic properties of the statistic

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Treating interest or groups the persons a corresponding anticomplementary malecule. The polyportides are useful for disponeing
preventing or treating turnor formation. Coults dissame, inflammatory
bowed ideases, food poisoning, malecules, degenerative dissame, betterial
miderions, accreticalists are also useful degreestive dissame, betterial
mainties, the polyportides are also useful doctries easily or for wound
mainties. The polyportides are also useful doctries and proper
and descepture from anti-polyment may be useful for trigging oals to the express
and the extension of the coult will be a formation of the county
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Sequence 1120 AA;

12; Gaps 64.2%; Score 256; DB 6; Length 1120; 72.0%; Pred, No. 1.38-22; ive 0; Mismatches 9; Indels 12 54; Conservative Query Match Best Local Similarity Matches

58 385 2 GLYYSANBQCRVAFGPKAVACTFAREHLDM --- CQALSCHIDPLDQSSCSRLLVPLLDGT 331 GLYYSANEQCHVAFGPPG-----CRLHLRQGAPCQALGCHTDPLDQSSCSRLLVPILDGT

386 ECGVERVHGRWSSWG 400

59 ECGVEK----WCSKG 69

AAU97642 standard, protein, 364 AA. AAU97642;

(first entry) Human Hea011374 protein. 27-AUG-2002

Aggrecanaes; osteopathio; antiarthritic; antiinflammatory; human; cartilage; osteoarthritis; inflammatory disease; enzyme; Hsa011374.

MO200233093-A2.

35-APR-2002

L7-OCT-2001; 2001WO-US032458.

18-OCT-2000; 2000US-0241469P. GEMY GENETICS INST

Agostino MJ, Wolfman NM, Morris EA; INC Twine NC, Racie LA.

WPI; 2002-454602/48. N-PSDB; ABK52580

Novel purified aggrecanase polypeptide useful for developing inhibitors and antibodies to the aggrecanase polypeptide, which are useful for treating aggrecanase-associated condition such as osteoarthritis.

Disclosure, Page 37-38, 41pp, English.

This invention calcase to the CROA and protein sequence of a snowl himma aggregation can calcase the protein of the invention may be used to minhate the protein calcase the protein of the invention may be used to minhate the of the invention may be used to minhate the of the invention is useful for developing inhibitors of aggregates protein a useful for developing inhibitors of aggregates protein when the contract of the invention is useful for developing the invention is useful for developing the invention of the invention is useful for developing the invention of the invention is the contract of the invention is useful aggregates and it of given calculations and the invention of the inventio

disorders incluying collisis. Cognisis of tissue disorders in which approximate is irregularly transcribed or expressed. The DN enquence and all the bureful for specialists of the gradient for great interpretability continued by Michigan States and States of the gradient of settlings by Disorders of the specialists of the gradient of settlings of DN Disorders and sembled for inhibitors of lits sortiety. An approximate profit inhibitors and sembled for inhibitors of lits sortiety are supported by the special of the states of the service of t Sequence 364 AA; 88888888888

60.7%; Score 242; DB 5; Length 364; Larity 97.7%; Pred. No. 26-21; Conservative 1; Mismatches 0; Indels Best Local Similarity Matches 42; Conserv Query Match

Gaps ..

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RESULT 13 ABP43989

ABP43989 standard; protein; 364 AA ABP43989;

Procellagen I N-proteinase (first entry) 26-PEB-2003

Neuropzocetivo; immunomidalaco; centece; droznosedes dely, oyocetali; allore; Albanacory; gene cherapy; nutritional supplement; wound; burn lunge; Albaniene's disease; Huntingorie disease; succionalization; anyocopia cherapia delecesis; aucoimmune diseode; inflammation;

valnerary

40200231111-A2 Sos taurus.

L8-APR-2002

11-CCT-2001; 2001WO-US027760. 12-0CT-2000; 2000US-00687527.

Asundi V, Zhang J, Zhao QA, Ren F, Drmanac RT; Zhou P, HYSE-) HYSEQ INC

Wehrman T, WPI; 2002-426278/45. Yang YT, Liu C, Xue AJ, Yang Y,

N-PSDB, ABQ61233

New polypeptides and their encoded proteins, usefil as nutritional acources or supplement or in gene therapy, particularly for treating wounds. Allahimer's disease, amportophic lateral solersale, cancer or inflammation

claim 20; SEQ ID # 892, 357pp + Sequence Listing, English.

The invention relates to of the fronty included polyhundicules sequences. The activity of polyhundicules de the invention may be described as white many included to the control of the co

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degradation of aggreean. The invention may be useful for the development of Theory the development of Engreeanse associated disorders, sends as a section of the property conditions. The present sequence as the amino acid sequence of the Instantant Sequence as the amino acid sequence of the Instantant Sequence as the amino acid sequence of the Instantant Sequence of the Instantant Sequence as the amino acid sequence of the Instantant Sequence and the Instantant Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises the article and and disting equation of a con-
Ni-liberad factor (WF) Clasting stayes. The SNS and protein sequence the invention are useful. In the disposite and research of the invention properties and research of the invention properties and research of the invention of the invention of the protein of the invention of the protein of the invention of the protein of the invention of the protein of the invention of the protein of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the inv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakadaki T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    von Wilderand factor-cleaving enzyme; thrombocycopanic purpura;
mycardial infarction; cerebral infarction; arteriosclerosis;
jaleblet thrombosis; stemosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; protease inhibitor; gene therapy; vWF-cleaving enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.7%; Score 242; DB 6; Length 1323; 97.7%; Pred. No. 8.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                            DB 7; Length 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEXMCSKGRC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hamamoto T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 IDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEXWCSKGRC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 LDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRC 71
                                                                                                                                                                                                                                                                                                                                                                                            Score 242; DB 7;
pred. No. 2e-21;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nozaki C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 112-121; 144pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAO16620 standard; protein, 1323 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maeda H,
                                                                                                                                                                                                                                                                                                                                                                                            97.74;
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27-JJL-2001, 2001JP-00227510.
26-SFP-2002; 200JP-00017596.
25-JAN-2002; 200JP-00017596.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MPI; 2003-120479/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABT32586
                                                                                                                                                                                                                                                                                                  Sequence 365 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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ASMRP1895 represent polyperidae encoded by polymucipenidae of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained alsocronic format directly from XIVO at fip. wipo.int/pub/pub/published por_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aggiecanae, aggredan articular carillage, protecglycian proteclytic; cardiage degradation; osteoarthritis; inflammatory joint (lesses and artaribities) degradation; osteoarthritis; inflammatory condition; aggredated discrete; osteoarthritis; inflammatory condition; aggredated discrete; osteoarthritis; inflammatory condition;
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                                                                                                                                                                                                                                                                                                                                          60.7%; Score 242; DB 5; Length 364;
97.7%; Pred. No. 2e-21;
.ive 1; Mismatches 0; Indels
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Les 42, Conserv
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                                                                                                                                                                                                                                                Seguence 364 AA.
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Search completed: March 13, 2004, 07:39:02 Job time : 11.3911 Secs

SEC NEWCQALSCHIDPLDQSSCSRLLVPLLDGTECGVEKMCSKGRC 322

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. - protein search, using sw model OM protein

March 13, 2004, 07:43:25; search time 5.62083 Seconds (Without alignments) 2667.199 Willion cell updates/sec US-09-836-712-2_COPY_124_394 399 1 POLYXSANEQCRVAPGPKAV......vPLLDGTECGVEKNCSKGRC 71 Title: Perfect score: Sequence:

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Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysas of the rotal score distribution.

SUMMARIES

Query Score Match Length DB

Description

Sequence 4. Ac	Semience 2. And	Sequence 2. An	Sequence 8. An	Seguence 11, An	Sequence 5, Apr	Segnance 5, At	Sequence 6, Ap	Seguence 8, At	Sequence 4, Ap	Sequence 10, A	Sequence 13, A	Seguence 20, A	Sequence 6, App	Semience 6. ar
US-10-222-334-4	US-09-836-712-2	US-10-222-334-2	US-10-057-487-8	US-09-781-080B-11	US-09-978-979-5	US-10-057-487-5	US-10-188-869-6	US-10-188-869-8	US-10-188-869-4	US-10-188-869-10	US-10-188-869-13	US-10-188-869-20	9-626-926-60-SD	TIS-10-057-487-6
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REMINISTED W10/202 RESULT 1 US-10-222-334-4

ORGANISM: Homo sapiens US-10-222-334-4 TYPE: PRT

301 PGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 360 1 PGLYYSANEQCRVAPGPKAVACTPAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 60 Gaps ó Ouery Match 100.0%; Score 399, DB 14; Length 842; Best Local Similarity 100.0%; Pracel No. 4.2e.39; Marches 71, Conservative 0; Mismatches 0; Indels 0;

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GVEKWCSKGRC 371 61 GVEKWCSKGRC 71 361 임 ò

RESULT 2 US-09-836-712-2 ; Sequence 2, Application US/09836712

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Deer Local Similarity 100.08; Pred. No. 746-39; 774-39; Matches 7; Conservative 0; Mismatches 0; Indels 0;
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SEQ ID NO 2
LENGTH: 1416
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Patent No. US20010049106A1
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US-09-836-712-2
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LENGTH: 1427
TYPE: PRT
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US-10-222-334-2
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301 PGLYYSANEQCRVAPGPKAVACTPAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 360
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                                                                                                                                                                                                                                                                                                                                 1 POLYYSANBOCRVAPGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 60
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64.24) Score 256, DB 9; Length 1120;
edget Local Similarity 72.04; Pred, No. 7.1e-22;
Matches 54; Conservative 0; Mismatches 9; Indels 12;
Matches 54; Conservative 0; Mismatches 9; Indels 12;
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                                                                                                                                                                                                                                           Query Match 100.0%; Score 399; DB 14, Length 1427; Best Local Similarity 100.0%; Pred. No. 7.44-29, Matches 71, Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Racie, Lisa, A.
TWIGE NSTAILS, C.
Aggesino, Michael, J.
Wolfman, Nell
WOTTE, Elisabeth
TITLE OF INVENTION: Aggrecatage Molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(1120)
OTHER INFORMATION: Xaa = Any Amino Acid
CURRENT FILING DATE: 2002-01-25
PRIOR PRILICATION NUMBER: 60/241,469
PRIOR FILING DATE: 2000-10-18
NUMBER OF SED ID NOS: 8
SOFTWARE: PATENTIN VERSION 3.1
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Sequence 11, Application US/09781080B

Patent No. US20020142439A1
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Patent No. US20020151702A1
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US-10-057-487-8
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Gaps ō

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1 PGLYYSANEQCRVAPGPKAVACTPAR -- EHLDMCQALSCHIDPLDQSSCSRLLVPLLDGT 58
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45.4%; Score 181; DB 14; Length 756;
Best Local Similarity 22.1%; Pred. Nov. 4.5e1.
Matches 28; Conservative 7; Mismatches 20; Indels 8; Gaps
Query Match

60.74; Score 242; DB 14; Length 365;
Best Local Similarity 97.74; Petd. No. 9.8e-21.

Matches 42; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.4%; Score 181; DB 14; Length 779;
                                                                                                                                                                                                                                                                                                            29 LDMCQALSCHTDPLDQSSCSRLLVPLLDGTECGVEKWCSKGRC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDMCOALSCHIDPLDOSSCSRLLVPLLDGTECGVEKWCSKGRC 43
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APPLICANT: BACTE LISA
APPLICANT: DIBLABIO, ELIZABETH
APPLICANT: AGOSTINO, MICHAEL
TITLE OF LIVERTION: AGOSTINO, MICHAEL
TITLE OF LIVERTION: AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO, AGOSTINO,
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10-10-189-669-6
5 Sequence 6, Application US/10188869
7 Publication No. US20030148306A1
6 GENRRAL INFORMATION:
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US-10-188-869-6
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LENGTH: 779
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US-10-188-869-8
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               NUMBER OF SEQUENCES: 6
CORRESPONDING ADDRESS:
ADDRESSEE American Home Products Corporation
STREET: One Campus Drive
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MARKE, REMINION, RILER J.
REGISTRATION WHERE 12,145
TELEPHONE: (1971) 650-500
TELEPHONE: (1971) 650-500
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TELEPHONE: (1971) 650-500
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-978-57
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NAME/KET: MISC_FEATURE:
COATION: (186]..(186)
OTHER: INFORMATION: unknown amino acid
US-10-637-487-6
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OTHER INFORMATION: unknown amino acid
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                                                                                                                                                                                                                                                                                                            CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
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221 PGMHYSANEQCQILFGMRA---TFCRNMEHL-MCAGIMCLVE--GDTSCKTKIDPPLDGT 274 331 PGWHYSANEQCQILPGMNA---TFCRNMEHL-MCAGLWCLVE--GDISCKTKLDPPLDGT 384 1 PGLYYSANEQCRVAFGPKAVACTFAR -- EHLDMCQALSCHTDPLDQSSCSRLLVPLLDGT 58 1 PGLYYSANEQCRVAFGPRAVACTFAR - EHLDNCQALSCHTDPLDQSSCSRLLVPLLDGT 58 B; Gaps Match 45.4%; Score 1817, DB 14; Length 807; Local Smilarity 52.1%; Pred. No. 4.6e-13; Local Smilarity 52.1%; Rismatches 20; Indels 8; Gaps 88 38; Conservative 7; Wismatches 20 Best Local Similarity 52.1%; Pred. No. 4.4e-13; Matches 38; Conservative 7; Mismatches 20; Indels Requests of Application (A) (A) Description (A TO THE SECOND TO THE SECOND SE PRIOR APPLICATION NUMBER: 60/149,133
PRIOR FILING DEE: 2002-01.16
PRIOR APPLICATION NUMBER: 60/303,051
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 3.1 275 ECGADKWCRAGEC 287 385 ECGADKWCRAGEC 397 59 ECGVERWCSKGRC 71 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 4 LENGTH: 807 59 ECGVERWCSKGRC 71 ORGANISM: Homo sapiens US-10-188-869-4 TYPE: PRT Query Match

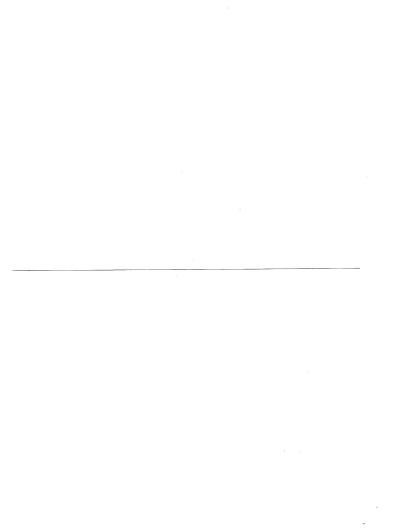
SEQ ID NO 10 LENGTH: 1057 TYPE: PRT ORGANISM: Homo sapiens

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401 PGMIYSANEQCQILFOMNA---TFCRNNEHL-MCAGIWCLVE--GDTSCKTKLDPPLDGT 454
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                                                                                                                                                                           Gaps
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Query Match 45.4%; Score 181; DB 14; Length 1057; Sear Local Similarity 52.1%; Pred. No. 6.18-13 Matches 38; Conservative 7; Mismatches 20; Indels 8; Matches 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 20; And 
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CHERNY FLIND NOTE: 20-70-5, 1018.69
PRIOR APPLICATION NUMBER: 60/349, 133
PRIOR PLIND NOTE: 200-2-1.6
PRIOR APPLICATION NUMBER: 60/349, 531
PRIOR PLIND NOTE: 200-5-1.6
PRIOR APPLICATION NUMBER: 60/340, 551
NUMBER OF SEQ 10 NOS: 314
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APPLICANT: BACTE, LISA
APPLICANT: BACTE, LISA
APPLICANT: AGGSTIVE, MICHAEL
TITLE OF INVENTION: AGGSTORANDE MOLECULES
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Publication No. US20030148306A1
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SEQ ID NO 13
LENGTH: 1122
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US-10-188-869-10

RESULT 15 US-10-057-487-6	Periltania Papilania Perilania Papilania Perilania Papilania			; SEQ. ID NO 6 ; LEWOTH; 738 ; TYEE: PRT ; ORGANISH: home sepien	FEBATURE I NAME/KEY: MISC_FEBATURE I LOCATION: 1(3): (43): (43) OTBER INFORMATION: unrinoun amino scid	FASTURE : NEGET FEATURE : NAME/KEY: NISC FEATURE : NOTATION: 1,102 : O'CHER INFORMATION: INFROME MAIND ACID	NAME/URS NICC PRATURE NAME/URS NICC PRATURE NOATION: (255). (255)	OTHER INFORMATION UNMINMENT STATE NAME/NEW MISC FEATURE COCKTON 1 258	GTHER INPORMATION: unknown amino acid FEATURE ANALYRE ANALYRE	LOCATION (374). (374) OTHER INPORMATION: unknown amino acid	NAME/KEY, MISC PEATURE) LOCATION: (397). (397)) OTHER INVERMENTON: unknown amino acid	FEATURE : NAME / KEY : MASC FEATURE : DAME / KEY : MASC FEATURE : LOCATION : (452) (452)	COTHER INFORMATION: unknown amino acid PERATURE: NAME/FORT: MISC PERATURE	LOCATION: (458); (458); OTHER INFORMATION: unknown amino acid	NAMP/KEY, MIGC FEATURE LOCATION: (475)	SEATURE: NAME/EERINGS SEATURE (CONTINUE NAME/EERINGS) (CONTINUE NAME/EERING SEATURE NA	United States United State	Oy 2 GLYYSANBOCKYAROPKANGTRABHL 29 0; DD 153 GLYYSANBOCKYAROPKANGTRABHL 180	Search complated: March 13, 2004, 08:07:04 JOb Lime : 6,62083 secs
; ORGANISM: Homo saplens US-10-188-869-20	Query Match 45.4%; Score 181; DB 14; Length 1145; Best Local Smilarity 25.14; Peted No. 67-13; Hell Matches 39; Conservative 7; Mismatches 20; Indels 8; Oaps	ON 1 PGLYYSANBOGNAROGRAN-CTRARBHIDWOOALSCHTDFLDOGSGGRLUVPLLDOT 58 10 466 PGHYSIANDCOLIFORMTPCRNORHL-WOOLWELVWGDFSCKTKLDFLDOT 519	Oy 59 BDGVEKNCSKORC 71 Db 520 FCMADKWCSKORC 532	KESUL 14 15-09-978-579-6	. Sequence 6, Application 198 (99978979 PAREAL INCOMPANY NO. USCOMPANY	Amine Natealis, C. Agostino, Michael, J. Adostino, Michael, J. McFman, Mishael, Mishah	TITLE OF INVENTION: AGGICCENES MOLECULES MANGER OF SEQUENCES. GORRESPONDENCE ADDRESS:	ADDARDERS: AMERICAN HOME FIGURATE OFFORTION FINEST: ONe Campus Drive CTATE: New Jersey STATE: New Jersey	COUNTRY: USA ZIP: OCOUNTRY: USA ZIP: OCOUNTRY: USA	CONTURED TANGED TOOL CONTURED TANGE TARGET AND CONTURED TO CONTURE TO CONTURE TO CONTURE TO CONTURE TO CONTURE TO CONTURE TO CONTURE TO CONTURE TO CONTURE TO CONTURE TO CONTURE TO CONTURE TO CONTURE TO CONTURE TO CONTU	SOTTWARE Fatentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/999,979 APPLICATION NUMBER: US/999,979	FILING DATE: 16-OCT-2001 CLASSIFICATION: «Unknown» PRIOR PAPLICANION DATA:	APPLICATION NUMBER: US/60/241,469 FILING DATE: -UDKNOWN: ATTORNEY/AGNT INCORMATION:	NAME: Kapinos, Ellen J. REGISTRATION NUMBER: 32,345 REPRENCE/DOCKEY NUMBER: 01 54350	TELECOMMUTCATION IMPORMATION: TELEPHONE: (973) 660-5000 TELEPHONE: (973) 683-4117	INPOMANTOR FOR BEQ. 10 NO. 6. SEQUENCE CHEARCETER: STICS: TATES amino acids TYPE: amino acid	STANDEDBESS unitnown STANDEDBESS unitnown MULBCILE TYRE protein SEQUENCE DBSCRIFTION: SEQ ID NO: 6:	Query Match 38.1%; Score 152; DB 9; Length 718; Bset Local Statlarity 100.0%; Pred. No. 1.509; Indels 0; Gaps Matches 28; Conservative 0; Missacches 0; Indels 0; Gaps	Oy 2 CLYVRANSCONYANCHRANCES 29 Db 153 GLYYSANSCONYANCHRANCH 100

LENGTH: 1145 TYPE: PRT



GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

March 13, 2004, 07:34:04 ; Search time 2.99531 Seconds (Michow alignmente) 122:37:72 Million cell updates/sec Run on:

US-09-836-712-2_COPY_324_394 Title: Perfect score:

1 PGLYYSANEQCRVAFGPKAV......VPLLDGTECGVEKWCSKGRC

Seguence: Searched:

389414 segs, 51625971 residues Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

SUMMARIES

	Appli	Appli	Appli	Appl	Appl	Appli	Appl	Appl	Appl	Appl	Appli	Appl	Appli	Appli	Appl	Appli	5, App	Appl	Appl	Appl	Appl	Appli	Appli	Appli	Appl	Appli	App11
c	'n	÷	7	ä	15	2	15,	15	16,	12	à	Ĕ	ò	ci	33	۲,	155	Ē	22	122	24	Ř	č	2	1,	œ	6
Description	Sequence	Seguence	Seguence	Segnence	Sequence	Sequence	Segmence	Sequence	Sequence	Sequence	Segmence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence
ID	US-09-491-522-5	US-09-930-872-4	US-09-369-364A-7	US-09-491-522-11	US-09-369-364A-15	US-09-369-364A-2	US-09-122-126B-15	US-09-634-286A-15	US-09-130-491-16	US-09-445-023A-12	US-09-445-023A-1	US-09-130-491-13	US-09-568-559-2	US-09-130-491-2	US-09-369-364A-22	US-09-491-522-7	US-09-800-729-155	US-09-369-364A-13	US-09-963-791-22	US-09-963-791-12	US-09-963-791-24	US-09-122-126B-2	US-09-634-286A-2	US-09-963-791-2	US-09-369-364A-17	US-09-130-491-8	US-09-369-364A-9
93	4	4	4	4	4	4º	4	4	4	4	4	4	4	4	4	4	4	4	4	*	*	4	**	**	4	4	٧
Query Match Length DB	1211	1224	997	1205	874	930	930	930	551	727	727	609	949	967	518	566	2165	1882	438	589	757	837	837	908	1081	481	905
Match	33.8	33.8	31.2	31.1	30.8	30.6	30.6	30.6	30.5	30.5	30.2	29.9	29.9	29.9	29.3	27.8	27.8	27.3	26.9	26.9	26.9	56.9	26.9	26.9	24.2	21.9	19.4
Score	135	135	124.5	124	123	122	122	122	121.5	121.5	120.5	119.5	119.5	119.5	117	111	111	109	107.5	107.5	107.5	107.5	107.5	107.5	96.5	87.5	77.5
Result No.	-	8	٣	*	S	9	7	60	6	10	11	12	13	14	15	97	1.1	18	19	20	21	22	23	24	25	26	27

RESULT 1

APPLICANT COLOR ALAIN
APPLICANT LABORER, CANADA AND APPLICANT LABORER, CANADA AND APPLICANT AND APPLICANT AND APPLICANT AND APPLICANT AND APPLICATION APPLICATION AND APPLICATION AND APPLICATION APPLICATION AND APPLICATION APPL COMPUTED TO STATE OF THE STATE 8389-0060-999 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/886,333 FILING DATE: US-09-491-522-5 US-09-491-522-5) Sequence 5. Application US/09491522 Patent No. 642898 GENERAL INFORMATION: ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 919
TELECOMMUNICATION INFORMATION: TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: 1211 amino acids TELEPHONE: 650-493-4935 650-493-5556 STRANDEDNESS: single TOPOLOGY: linear amino acid CLASSIFICATION: CITY: New YOR STATE: NY COUNTRY: USA LENGTH:

2 Query Match 33.84; Score 135; DB 4; Length 1211; Best Local Similarity 45.18; Pred. No. 58-08; Matches 32; Conservative 5; Mismetches 32; Indels Matches 32; Conservative 5; Matches 32;

Gaps

182 PGIHYSNAREQCREDEGLGYNACTAFRI-FDPCKQLMC-SHPDNPYFCKTKKGPPLDGTMC 539

CURRENT APPLICATION NUMBER: US/09/930,872
CURRENT FILMS DATE: 2012-08-14
PRICE APPLICATION NUMBER: US 60/225,852
PRICE FILMS DATE: 2000-08-16
NUMBER OF SEQ 1D NOS: 5
NUMBER OF SEG 1D NOS: 5
OCTWARS: PRESESS for Windows Version 4.0

TYPE: PRT ORGANISM: homo sapiens

US-09-930-872-4

Query Match

SEQ ID NO 4

US-09-300-872-4 US-09-300-872-4 ; Sequence 4, Appl.cation US/09930872 Patent No. 644838

540 APGKHCFKGHC 550

61 GVEKWCSKGRC

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PGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVFLLDGTEC 60

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1 PGLYYSANEQCRVAPGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 60
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                                                                                                                               APPLICANT. Lapiece, Charles N.
APPLICANT. Lapiece, Charles N.
APPLICANT. Lapiece, Charles N.
1711L GO INVENTION. RECOMBLANT N-PROTEINAS,
TITLE OF INVENTION. RECOMBLANT N-PROTEINAS,
NOTITIES OF INVENTION. RECOMBLANT N-PRO
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Brobakan, Tiina L.
Brobakan, Astoshi
VENTION: Nucleic Acids Encoding Zinc Metalloproteases
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Pred. No. 1.1e-06;
5, Mismatches 33, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 8389-0060-999
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CURRENT APPLICATION NUMBER: US/09/369,364A
                                                                                                                                                                                                                                                                                                                                                                                                               E: Pennie & Edmonds, LLP:
1155 Avenue of the Americas
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Patent No. 6391610
Sequence 11, Application US/09491522
Patent No. 6428998
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 650-493-4935
TELEPAX: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskelu
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
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Best Local Similarity 43.7%;
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GVEKWCSKGRC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036-2811
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si:
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APPLICANT: Hirohata,
TITLE OF INVENTION: 1
FILE REPERENCE: 2647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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APPLICANT: Apre, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-369-364A-15
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US-09-491-522-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                           GORREAL, NYROWSKYCH CH. JOHN
THIRD CH. PREFERENCE CH. JOHN
THIE OF PREFERENCE LEV. CO. 1543-054 RHAMEN Processes and Polymucleorides Enceding the Sa
THIE DEPREFERENCE LEV. CO. 1513-154.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508 PGELYDANTOCKWOFGEKAKLCMLDFKK-DICKALWCHR---IGRKCETKFWPAAEGTIC 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 PGLYYSANBQCRVAFGPKAVACTFARBHLDMCQALSCHTDPLDQSSCSRLLVPLLDGTEC 60
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Sequence 7, Application US/09369364A Patent No. 6391610

US-09-369-364A-7

564 GHDMWCRGGOC 574

61 GVEKWCSKGRC 71

ORGANISM: Homo sapiens ADAMTS-7

PRT

JS-09-369-364A-7

60 CGVBKWCSKGRC 71

g

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487 PGOTYDATOČNLTFGPEYSVČ----PGMDVČARLMČAVVROGÓMVČLTKKLPAVEGTPC 542
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APPLICANT: Goodearl, Andrew J.
APPLICANT: Goodearl, Andrew J.
APPLICANT: Goodearl, TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
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           Query Match 30.6%; Score 122; DB 4; Length 930; Bet Local Similarity 33.8%; Pred. No. 1.44-06. Matches 44; Conservative 11; Mismatches 32; Indels Matches 44; Conservative 11
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BRALIER PAPLICATION WHOREN: US 64/054,961
BRALIER PLIANCE DATE: 1997.08-06
SUPPLASS: FARESO DO WINDOW WEREION 3.0
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US-09-634-286A-15
; Sequence 15, Application US/09634286A
; Patent No. 652436
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US-09-130-491-16
; Sequence 16, Application US/09130491
; Patent No. 6416574
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Best Local Similarity
Matches 24; Conserv
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LENGTH: 551
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Best Local Similarity 33.84; Pred. No. 1.4e-06. 
Matches 44; Conservative 11; Mismatches 32; Indels
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Patent No. 6451575
GENERAL INFORMATION:
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus ADANTS-9
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ORGANISM: mus musculus ADAMTS-5
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US-09-122-1268-15
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LENGTH: 874
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DD 62 POTIONARQOPPORRESHEPAASTUTIACTORREGAL/VOCAMEPANOTISC 118 OV 61 POTROCHARGE 71 DD 1110 despectivent 129 MASUL 12, 120 MA	No. 9-645-023-12 Control COV-9445923A Spring A. State Cov. 1 Control Cov. 1 Control Cov. 1 C	Qurry National Sailarity 15-51 Score Score 15-51 Score Sailarity 15-51 Score	MESTER 11. 10. 10. 10. 10. 10. 10. 10. 10. 10.

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Query Match

29.3*; Score 117; DB 4; Length 518; Best Local Similarity 33.88; Pred No. 3e-06; Matches 34; Conservative 9; Mismatches 34; Indels
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Job time : 3.99531 secs
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Patent No. 6391610
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Patent No. 6416974
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A.Roselder (1988 AND) F)481-547/Domain: thrombospondin type 1 repeat homology «THR3» F)551-581/Domain: EQR homology «EGR P. F)248-356,708,106/Staffing Eles: carbohydrate (Asn) (covalent) #status predicted thrombospondin precursor - chicken CiSpecies Gallus gallus (chicken) CiDece 10-6ep-1999 Heaquence_revision 10-Sep-1999 #text_change 10-8ep-1999 503 WGPWSPWSACTVICGGGIRERSRICNSPEPQYGGKPCVGDTKQHDWCNKRDC 554 495 WGPWSPWDICSVTCGGGVQRRSRLCNNPTPQFGGKDCVGDVTENQVCNKQDC 546 1 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQAC 52 1 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQAC ch 43.8%; Score 160; DB 1; Length 1178; 1. Similarity 48.1%; Pred. No. 2.2e-09; 25; Conservative 8; Mismatches 19; Indels Length 1170; Query Match 44.1%; Score 161, DB 2; Length 1179
Beet Local Similarity 51.9%; Pred. No. 1.7e-09; Indels
Matches 77; Conservative 5; Mismatches 20; Indels CjAccession: Å59804 Ritakler, J. Duggette, M.; Perro, P. 2101. Chem. 266, 8039-8043, 1591 A.Affille (Coning and eeqenerich) A.Reference number: A39804; WID:91217036; PMID:0222631 thrombospondin 2 precursor - mouse Query Match Best Local Similarity Matches 25; Conserva A:Accession: A39804 RESULT 6 ò 용 A Stebuse Pyes DNA
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44.1%; Score 181; DB 1; Length 1170;
Best Local Similarity 51.9%; Pred. No. 1.78-09;
Best Local Similarity 51.9%; Fred. No. 1.78-09;
Matches 27; Conservative 5; Mismacches 20; Indels 4 A,Status: preliminary, not compared with conceptual translation A,Molecule type: mRNA A, Cross-references: GB:M87276 A,Status: preliminary A,Molecule type: DNA A; Accession: A37905

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60 MSQQC 64
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Fi456-692/Domain: thrombospondin type 1 repeat homology «THR2»
Fi353-548/Domain: thrombospondin type 1 repeat homology «THR3»
Fi353-581/Domain: ESF homology &ESFs.
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ö Gaps .. ch 42.7%; Score 156, DB 2, Length 1172; 1. Similarity 46.2%; Pred. No. 5.9e-09; 1. Similarity 10, Mismatches 18; Indele 18; J. Conservative 10, Mismatches 18; Indele Sest Local Similarity Matches 24; Conserv Query Match

CiSpecies: Homo sapiens (man.) C.pate: 20-apr-2000 #seguence_revision 20-apr-2000 #text_change 20-Apr-2000 C.Accession: TATA hypothetical protein DKF2p762C1110.1 - human (fragment)

R.Blum, H.; Baudersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.; submitted to the Protein Sequence Database, March 2000 A.Reference number: 224379 A;Status: preliminary A;Nolecule type: mRNA A;Residues: 1-550 cAAA> A;Cross-references: BNBL:AL162080

A, Experimental source: adult melanoma (MeWo cell line), clone DXFZp762C1110

.Match 42.6%; Score 155.5; DB 2; Length 550; Local Similarity 41.5%; Prefed, No. 3.76-09; All 166 17; Conservative 9; Mismatches 26; Indels 3. A; Note: DKFZp762C1110.1 Query Match

1 WSSWGPRSPCSRSCGGGVV/TRRRCCNNPRPAFGGRACVGADLQAEMCNTQAC-EKTQLEP 59 Gaps

145 WGWNGPWGDCSRTCGGGVQYTWRECDNPVPKNGGKYCEGKRVRYRSCNLEDCPDNNGKTF 204

60 MSQQC 64

205 REEQC 209

gene ADAMTS-1 protein - mouse

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A,Cross-references: EMBL:AB001735; NID:g2809056; PIDN:BAA24501.1; PID:g2809057 A,Experimental source: strain 1295VJ Aintrons: 228/1; 343/3; 388/1; 444/1; 539/3; 602/1; 660/3; 719/2 Sisuperianily: thrombospondin type 1 repeat homology cTHR3> F:542-589/Domain: thrombospondin type 1 repeat homology cTHR3> Gene: ADAMTS-1

1 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQAC-EXTQLEF 59 Ouery March

12 (4) Soore 155 5, DB 2, Length 951;
Bost Local Similarity 41.54; Pred, No. 5.7e-06.2

Matches 27; Conservative 9, Mismatches 28; Indels 1; Gaps

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546 WGPWGPWGDCSRICGGGVQYIWRECDNPVPKNGGKYCBGKRVRYRSCNIEDCPDNNGKTF 605

506 REEQC 610

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Nypothetical protein XIAN0689 - human Species: Hono appleas (Ames) appleas (Ames) CINECO (CINECO panies of the Compan

c;Superfamily: thrombospondin type 1 repeat homology <THR3>

42.3%; Score 154.5; DB 2; Length 837; 43.1%; Pred. No. 6.5e-09; Indels 6; Mismatches Best Local Similarity 43.19 Matches 28, Conservative Query Match

1 WSSWGPRSPCSRSCGGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEK-TQLEF 59 523 WGPWGPWGDCSRTCGGGVQPSSRDCTRPVPRNGGKYCEGRRTRPRSCNTEDCPTGSALTF 582 60 MSQQC 64 윱 à

C.Species: Canoninabdatis elegans C.Species: Canoninabdatis elegans C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 nypothetical protein F25H8.3 - Caenorhabditis elegans

583 REEQC 587

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RESULT 11

submitted to the EMBL Data Library, February 1996 A;Reference number: Z19413 C.Accession: T21371; T24896 R:Gajadsty, S. A,Accession: T21371

Aydagenie "politikaay, translated from GB/RMEL/DDBJ Aydagenie type: DDBJ A/Rosidues 1516 * MIL-265360; PIDN:CAN93287.1, GSPDB:GM0022, CESP:F25H8.3 R.Galadsty, S. submitted to the EMBL Data Library, February 1996 ; Experimental source: clone F25H8

A, Residues: 1-2165 -W12> A, Cross-references: EMBL; 269361, PIDN:CAA93288.1, GSPDB:GN00022, CESP:P25H8.3 A.Reference number: Z19949 A.Accession: T24896 A.Status: preliminary; translated from GB/EMBL/DDBJ Experimental source: clone T13H10 A.Gene: CESP: F25H8.3 A; Molecule type: DNA

A;Map position: 4 A;Introne: 31/1; 52/1; 135/2; 193/3; 216/1, 266/1, 495/2; 547/3; 584/3; 634/2; 744/1;

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Shilarity 40.6%; Score 140.5; DB 2; Length 1559; CShilarity 40.6%; Pred. No. 3.46-07; Conservative 9; Mamacrdes 20; Indels 9; Gape 22; Conservative 9; Mamacrdes 20; Indels 9; Gape

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RESULT 15

RiGeisel, C., Bradshaw, H. submitted to the EMBin Date library, July 1996 submitted to the EMBin Date library, July 1996 Alpescription: The sequence of C. elegans cosmid C37C3. AlReference number: Z21518 Accession: T34395

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!- SIMILARITY: Contains 6 TSP type-1 domains !- SIMILARITY: Contains 1 PLAC domain.

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. domo sapiens (Human)

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Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A., MEDLINE=20396138; PubMed=10936055; TISSUE-Fetal

Maki R.A.; **ADAMTS 9, a novel member of the ADAM-TS/Metallospondin gene SEQUENCE FROM N.A. (ISOFORM 1), AND FUNCTION family."; Genomics 67:343-350(2000).

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Gaps '0 %; Score 185; DB 1; Length 1205; %; Pred: No. 3.7e-13; 10; Mismatches 23; Indels 50.7%;

RESULT

ATS2 BOVIN ID ATS2 BOVIN AC P79331,

PRT; 1205 AA STANDARD:

is-GT7.2001 (Rat., Q. Learesch).
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Bukaryota, Weiazoa, Chordata, Craniata, Vortebrata, Eutaleostomi, Mammalia, Eutheria, Pacestriodactyla, Ruminantia; Pecora, Bovoidea, Bordada, Bovinae, Bos. NCBI TaxID=9913;

SEQUENCE FROM N.A. TISSUE-Skin;

MEDIZISTERO, DARGAGISTERO, AL., NUSBRIN B.V., Prockop D.J., Calder, A. Li S.W., Eistero A.L., Nusbrin B.V., Prockop D.J., Calder C.W., and upperfected of Dornam probabilism. The proteinate a man embedre of the uppersently of time metalogic processing and the processing of time of the processing of t

PARTIAL SEQUENCE. MEDLINE-95348096; PubMed=7622483;

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This series more mary is copyright. It is produced through a collaboration the wheen the Assiss institute of Sichifornies and the PBE outselftion. There are no restrictions on its use by moreover institutions at long as is contained for connectiation and long as is contained for connectiation for the contained for connectiation for the contained for connectiation and the contained for connectiation and the contained for connectiation and the contained for connectiation and the contained and contained as con

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Pred. No. 1.18-12;
8; Mismatches 26; Indels 0; Gaps
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Characterization of DAMYE's and ADAMYE's as a distinct ADAMYE
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Memmellas Butheria, Primates Catarrhini, Hominidae, Homo.
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BY SIMILARITY.
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TSP TYPE-1 3.
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Best Local Similarity 46.9%;
Matches 30; Conservative
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IEGGÉESSE10-2: SEQUENCE-WES COUTGE, USE 070107, WES COTTOS.
IEGGESTECTIVE Very sparingly expressed, although is detected at low levels in tenefie, proteste ovary, heart, placenta, lung and pancreas. Overexpressed in several brain, colon and brasst

Event-Alternative splicing, Named isoforms=2;

IsoId=P59510-1; Seguence=Displayed;

-!- PTM: The precursor is cleaved by a furin endopeptidase (By

carcinomas. Name=2;

TISSENCY.

TO ACCUSATE THE PROPERTY OF THE PRO

Subfamily related to Caenorhabditis elegans GON-1."; J. Biol. Chem. 278:9503-9513(2003).

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49.6%; Score 181; DB 1; Length 1911; 45.3%; Pred. No. 1.6e-12; Live 9; Mismatches 26; Indels 0; Gape 1911 AA; 214656 MW; CF592E220D32B250 CRC64; Query Match Best Local Similarity 45.34 Matches 29; Conservative SEQUENCE

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Homo sapiens (Human). Bukaryotes Metazos; Chordata; Craniata; Vertebrata; Buteleostomi; Asmaalia, Butheria; Primates; Catarrhini; Hominidas; Homo. KCBL_TAXID=5606; ADAMTS15.

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similarity)
--- FTM: The precursor is cleaved by a furin endopeptidase (By
similarity).

-- SIMILARITY: Belongs to peptidase family M128. -- SIMILARITY: Contains 1 disintegrin-like domain. -- SIMILARITY: Contains 3 TSP type-1 domains.

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EMBL, AJ315733, CAC86014.1; -. MEROPS, M12.025; -. Genew, HGNC:16305; ADAMTS15.

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N-LINEED GLOCAC...) (FOTERITAL). Score 177; DB 1; Length 950; Fred. No. 2.4e-12; 8; Mismatches 26; Indels MW; SDFBE18285CCC3B CRC64; Sat Mar 13 0/:56:25 2004 48.5%; 103286 Query Match Best Local Similarity 45.57 Warrhes 30, Conservative STANDARD; 3461 3461 3461 3461 541 5623 361 362 362 371 141 591 623 679 679 579 PREBOC 584 59 FMSQQC 64 ATS2 HUMAN 095450; METAL ACT_SITE METAL METAL CARBOHYD CARBOHYD SEQUENCE RESULT 11 REFERENCES ò

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matrix (By similarity).
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This sitting and marry is copyright. It is produced through a collaboration the between the agests intertuce of distributions as done between the shortcommatter and the Bigg constation the burceau and solutionsation function. There are no restriction on its may by non-poptic instructions as done as its concerns is into way modified and this extensor is not removed. Usage by and for commercial entry of the configuration allocated produces a license agreement (see http://www.isb-sho.ch/shnounce/of-end on marrial to itemseable-sho.ch).
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Agorqiadis, X.E., Histolylate S. S. Galdin N.F., Aptre S. S.;
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--- Downlin The spacer domain and the TSP type-1 domains are important for a tight interaction with the extracellular matrix (By similarity).
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Bikaryota, Mecasoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bommania, Butheria, Primates, Catarrhini, Hominidas, Homo.
NCBI TaxID=9606;
413 440 YLTELLDGGHGDCLLDAFGAALFLPTGL
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890 Aa, 96671 NM; 57D70EE03D5739D3 CRC64,
                                                                                                                                                                                                               Query Match 47.1%; Score 172, DB 1; Length 890 Best Local Similarity 43.8%; Fred. No. 8e-12. Makefess 28; Conservative 9; Mismatches 27; Indels
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-- SIVILARITY: Belongs to peptidase family M12B.
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RESULT 15 SMSA_HUMAN

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Search completed: March 13, 2004, 07:39:57 Job time : 2,33333 8ecs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 54.0%; Score 197; DB 11; Length 900; Septe Local Stmllarity 46.4%; Pred 1 No. 9.18-17; Indels 0; Gaps Matches 2; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bijoliskistik.
Was mandrale (Nobel and Anthropistik) Skrayces, Marchelosten, Buteloostomi, Skrayces, Messay Chordaes, Craniatas, Vertebrata, Buteloostomi, Mammalia, Butheroptes, Messay Chordaes, Schurograthi, Muridae, Musinae, Mus
                                         Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, Scrambers, 
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SEQUENCE 900 AA; 100679 NW; 590BE2B0B73740FF CRC64;
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10-MAR-2003 (TERMELTEL, 23, Last sequence update)
01-07-2003 (TERMELTEL, 25, Last annotation update)
Mypotherical metalioprofesse.
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SEQUENCE FROM N.A.
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Homo sapiens (Human). Madrayota, Metazoa, Chordata, Cramiata, Vertebrata, Bureleostomi, Nammalia, Burienta Primates, Catarrhini, Hominidas, Homo.

01-DEC-2004 (TERMELTEL 19, Created)
01-DEC-2004 (TERMELTEL) 19, Created)
01-OCT-2003 (TERMELTEL) 25, Last annotation update)
01-OCT-2003 (TERMELTEL) 25, Last annotation update)
ADAMTELS

PRT; 1427 AA.

PRELIMINARY:

0961.37 RESULT 2

096137

119 8000 122

61 SQQC 64

Pubwedalissiya6, Zineng X., Ching D., Tekayama T.K., Majerus B.M., Sadler J.B., Liskawa K.;

SOLITA MANAGEMENT CON CONTRACTOR

SECUENCE FROM N.A.

VCBI_TaxID=9606; LISSUE-Liver

Journal (Mouse).
Blassycks, Metacos; Chordera; Craniara; Vertebrata; Buteleostomi;
Mammasia; Entheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL TaxID=10090;

Last sequence update)

01-OCT-2002 (TERMBLE-1, 22, OL-OCT-2002 (TERMBLE-1, 22, OL-OCT-2003 (TERMBLE-1, 25, Hypothetical protein. PRELIMINARY,

Q8X206 Q8X206;

RESULT 3 Q8X206 Created)

Ouery March 100.0%; Score 365; DB 4; Length 1427; Best Local Saniarity 100.0%; Pred. No. 38-38; Soniacryative 0; Mismatchies 0; Indels 0; Gaps Matchies 6; Conservative 0; Mismatchies 0 CHAIN 75 1427 VON WILLEBRAND FACTOR-CLEAVING PROTEASE. SEQUENCE 1427 AA; 153632 MW; EBIBC3AABC1A4442 CRC64;

POTENTIAL

Protease; Signal.

LUNET

Query Match

Best Loc Matches

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Children C. W., Addam N., Toromallace F.O., Erandon R.O., Footes V.,
Board C. A., Coccywe J. D., Amanatdes F.O., Erandon R.O., Footes W.,
Barroot J. A. H. H. Hadden D., Barroot J., Besen D. M.,
Barroot J. A. H. H. Hadden D., Barroot J., Besen D. M.,
Barroot J. A. H. Hadden J. B. A., Besen D. M.,
Berliese S. Faries E. Gulla R. F. (1967 N. Googles D.,
Berliese S., Faries E. Gulla R. F. (1967 N. G.) Googles D.,
Berliese S., Faries E. Gulla R. F. (1967 N. G.) Googles D.,
Berliese S., Faries E. Gulla R. F. (1967 N. G.) Googles D.,
Berliese S., Faries E., Berlin R. F., Hostin D., Hooland T.J.,
Berliese S., Faries E., Berlin R. F., Hostin D., Waller B. M.
Bollowson W. (1987 N. Berlin S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Faries S., Far
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                                                                                                                                                                                                                                                                 01-MAY-2000 (TEBNBLrel. 13, Created)
01-0CT-2002 (TEBNBLrel. 22, Last sequence update)
01-0CT-2003 (TEBNBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
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                                                                                                                                                            CG4096 protein.
       ò
                                                                                                                                                                                                           120 WSAMSKWSECSRICGGGVKFQERHCSNPKPQXGGKYCPGSSRIYKICNINPCPENSLDFR 479
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                                                                                                                                                            1 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAPGGRACVGADLQAEMCNTQACEXTQLEPM 60
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                                                                                     0, Gaps
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Deperture of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
51.2%; Score 187; DB 11; Length 1092;
45.3%; Pred. No. 2.2e-15;
tive 13; Mismatches 22; Indels 0
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popoters Endopeerygota; Dipera; Brachycera; Muscomorpha; 
Epiydroides; Drosophilidae; Drosophila; 
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.4%; Score 173; DB 5; Length 769;
45.3%; Pred. No. 9.8e-14;
tive 11; Mismatches 24; Indels
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VY119538; AAMS0192.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22, Created)
22, Last sequence update)
25, Last annotation update)
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PROSITE, PSS0092; TSP1; 1.
PROSITE, PS00142; ZINC PROTEASE; 1.
                                       Local Similarity 45.3%
nes 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.3%
Matches 29; Conservative
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01-OCT-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                      180 AQQC 483
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Submitt EMBL, A

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RESULT Q8MRLS

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SECUENCE

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631 WGDWSEWSEGSRSGGGGGGSTSTONPVPANGCVPCIGERKRYKICKRPCPAEEPSFR 690
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50.0016, A302-600. CAC(778-01.)

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Nomi-Tax/De5069.
Variable (P. 1999) C. V. Danishe C. S. Potoniki S. B. Sanish C. D. Diny J. L. Sergeno C. Serson B. Correct O. W. Cellifer S. B. Strong C. Diny C. Correct O. W. Cellifer S. B. Serson B. Correct O. W. Cellifer S. B. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C. Serson B. C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
EMBL, ROOG435; AAA44665.2; -...
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01-DEC-2001 (TERMELTE). 19, Last sequence update)

01-OFC-2003 (TERMELTE). 15, Last amotation update)

Epulin-6 (Fessment).
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TISSUE=Melanoma;
Kostka G., Timpl R.;
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1684 WSAWQPWGTCSESCGKGTQTRARLCNNPPPAFGGSYCDGAETOMQVCNERNC 1735
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Bukasyota; Wetazota Chordata; Cranista; Vertebrata; Euteleostomi;
Mammalia; Euthekia; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQAC 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2673;
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Local Similarity 55.8%; Pred. No. 4.5e-13;
nes 29; Conservative 5; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 1
2673 AA; 291017 MW; BEAEC30B8340E272 CRC64;
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01-DEC-2001 (TERMELRE): 19, Last sequence update)
01-CCT-2003 (TERMELRE): 25, Last annocation update)
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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516 WGPWIPWGDCSRSCGGGVSSSRHCDSPRPILIGGYYCLGERRRHRSCWINDCPPGSQDFR 575
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46.6%; Score 170; DB 11; Length 1070;
Best Local Similarity 43.8%; Pred, No. 3.38-13;
Matches 28; Conservative 7; Mismatches 29; Indels 0
Matches 28; Conservative 7; Mismatches 29; Indels 0
                                                                                                                                                                                                                                                                                                                                                                    4; Length 5636;
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                                                                                                                                                                                                                                                                                                                                                                    Query Match 47.15; Score 172; DB 4; Length 56; Beet Local Smilarity 55.8F; Pred. No. 9.38-13; Matches 29; Conservative 5; Wismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last amnotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY:
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                                                                                                                                                                                                                  Dronophila melanogaster (Fruit fly).
Bharyota Messon Afrikhopoda Heaspoda insecta) Ferrygota.
Ropersa, Endoperygota; Diptera Erschyoera, Mesconophia;
Bhydrodan Incompiliade; Drosophila.
                                                                                   01-UNN-2002 (TrEMBLrel. 21, Created)
01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
01-COTT-2003 (TrEMBLrel. 21, Last sentetion update)
GH153939 (CG14669 protein).
                               PRT: 1688 AA
                                      PRELIMINARY
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                                                                      Q8SXB0; Q9VF61,
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081183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signment STRON N. Matthews 3.8. Bayraktargalu i. Caraball N., Maras S. Crosby N.A., Matthews 3.8. Bayraktargalu i. Caraball N., Maras S. Crosby P. Manual C. Marasha R. S. Carlon J. W. Carabartar S. E. C. Caraba M. Toryadia R. Sament D. Fries E. d Grey J. Martin N. Kormilla S. Mariballa B. Millond D. Fries E. d Grey J. Rasso S. Kormilla B. Millond B. Mariballa J. Millond D. Robert C. Rasso S. Mashare R. J. Sament D. W. Marasha M. Maria M. Maria M. Maria M. Maria M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha Marasha M. Marasha M. Marasha M. Marasha M. Marasha M. Marasha
Associated W. Roschie W. Nostrino P. Woldand C.J., Thompson C., Jahli M. Krine D. id P. Welson E. Wohlfrelf A., Integens C., Jahli M. Krine D. id P. Welson C. Welson E.A., Namoo J., Bellob J., Bergess W., Barth S., Nelson C., Bellob E.A., Namoo J., Bellob J., Bergess W., Barth S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Petel S., Pete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEDURNICE FROM N.A. A. Adams M.D., Rubin G.M., Venter C.J.; Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the BMSL/GenBank/DDSJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.0%; Score 168; DB 5; Length 1688;
43.8%; Pred. No. 9.4e-13;
tive 8; Mismatches 28; Indels
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0.-1962-2003 (TERMELPE). 23, Last sequence update)
0.-007-2003 (TERMELPE). 25, Last sequence update)
AMANTA-120 predution (Fragment).
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                                   AAU97642 standard; protein; 364 AA
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N-PSDB; ABK52580.
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Wehrman T, Drmanac RT;
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100.0%; Pred. No. 3.38-31;
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Misc-difference 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD94035 standard; protein; 365 AA.
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Segmence 365 AA:
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0, Gaps
100.0%; Score 365; DB 7; Length 365; 100.0%; Pred, No. 3.3e-31; cive 0; Mismatches 0; Indels 0
                                        64; Conservative
                    Best Local Similarity
Matches 64; Conserv
    Query Match
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119 SOOC 122

61 SQQC 64

8

RESULT 4 AAU7921

AAU79217 standard, protein, 933 AA. Human ADAM-TS-like protein. (first entry) 15-JUL-2002

Member, ADMY-STIKE procedule, carticomentar disorder, angina, vascular speten, consequente disorder, sincercitor, inchestrator, statutes procedular infarction; inchestrator diseases; artichtusis, prepartentavo vascular diseases; ascondary arterial hypertenison; pertiperal vascular diseases; emboliar chickente propertenison; pertiperal vascular diseases; ance arterial thrombosis, nitiamestory vascular disorder; ottoric observative pulmonary diseases.

disorder

WOZ00226999-A2 fomo sapiens.

34-APR-2002.

86-SEP-2001, 2001WO-SP011124. 28-SEP-2000, 2000US-0235881P. 25-JUL-2001; 2001US-0307393P.

(FARB) BAYER AG Ciao Y;

MPI; 2002-383274/41. 4-PSDB; ABK49356.

New purified human ADAM-TS-like protein, useful for identifying modulators of protein activity for treating cardiovascular or liver Misorder or chronic obstructive pulmonary disease.

Claim 25; Fig 2; 106pp; English.

polymucleotide encoding it. The protein of the invention is useful for treating catdiovescular disorders including diseases of the heart and vascular system, such as congestive heart failure, myocardis, infarction, The invention relates to a human ADAM-TS-like protein and the

stokement Danard Classess or Gg, stells and ordinin, unstable and maintain a critical and ordining and ordinate and ordining and ordining and ordining and ordining and ordina 88888888888888

Length 933, 0; Indels 100.0%; Score 365; DB 5; 100.0%; Pred. No. 8.3e-31; 0; Mismatches 64; Conservative Query Match Best Local Similarity Matches

Sequence 933 AA;

Gaps

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8 ò 8

AA016618 ğ

Human von Willebrand factor (vWF) -cleaving enzyme-related protein #5 AAO16618 standard, protein, 1297 AA. (first entry) 15-MAY-2003

Human, procease inhibitor, gene therapy; vWF-cleaving enzyme; von Wilabrand factor-cleaving enzyme; thromborytopenic purpura; wycardial infaction; derebral infaction; arteriosclerosis; olatelet thrombogis; stenosis.

Homo sapiens.

W0200288366-A1. 07-NOV-2002

KAGA) CHEMO-SERO-THERAPEUTIC RES INST 25-APR-2001; 2001JP-00128342. 27-ULL-2001; 2001JP-00227910. 28-SEP-2001; 2001JP-0032997. 25-JAN-2002; 2002JP-00017596.

25-APR-2002; 2002WO-JP004141.

Hamamoto T, Nakagaki T; Soejima K, Mimura N, Maeda H, Nozaki C, WPI: 2003-120479/11. N-PSDB: ABT32584

von Willabrand factor-Cleaving enzyme, applicable in disqunsis of, and supplementary therapy for, thrombotic thrombotycopenic purpura, and feveloping drugs for e.g. myocardial infarction and cerebral infarction. Claim 4; Page 92-101; 144pp; Japanese.

The invention comprises the mains acid and coding sequence of a von Millachand factor (wPP)-cleaving enzyme. The DNA and protein sequence of this invention are useful, in the disapposis and treatment of this compoundation purpura, and in developing drugs for mycoxadial.

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the intensition statement on an absoluted or mainstraintilly pure to we Milhokrand factor-cleaving processe (WF-CP) polygetide, WF-CP de useful for a black of the factor-cleaving processe (WF-CP) polygetide, WF-CP de useful for a black of the factor cleaving the statement of the polygetide lise on the liberal contacting a black of the polygetide lise of the liberal contacting the will be polygetide lise of the liberal cleaving the will be polygetide lise of the liberal cleaving the will be polygetide lise of the liberal cleaving the will be polygetide and the polygetide lise of the liberal clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear clear cle
                 Novel isolated or substantially purified von Willebrand factor-cleaving protease, useful for producing preparation for therapy of thrombosis and biromboembolis of disease such as thrombotic thrombosytic purpura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mindran, Von Will-berband festor-cleaving processes vMF-cp; heregy; anaymes
transgerid animal; immunisation; thromboembolid diseases precelampsis,
thrombolid thromboytic purpurs; PTF, Panoch-Schonlain purpurs;
htrombolis; ngonatel thrombocytopenia; hasenolytid-ursamic syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Von Willebrand factor-cleaving protease fragment #2.
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Kerschbaumer R, Tagliavacca
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Best Local Similarity 100.08; Pred: No. 1.2e-30;
Best Local Similarity 0, Mismatches 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                             AAB24449 standard; protein; 1353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 64-68; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-2001, 2001WO-EP013391
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r F, Antoine G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic, anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4PI; 2002-479950/51
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                                                                                                                                            61 SQQC 64
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augulementary therapy for thrombocit chrombocytopenic pupus, and for
devaloping drugs for e.g. myocardial infarction and cerebral infarction.
infarction, cerebral infarction, arteriosclarosis, plateler thrombosis, and senosis. The present amino acid sequence represents a human von Allabrand factor (WRP)-cleaving enzyme-related protein
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yon Willabrand Eactor-cleaving enzyme, thrombocycopenic purpura,
yocatdial infarction, cerebral infarction, arteriosclerosis;
platelet thrombosis; secnosis.
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                                                                                                                                                                         Length 1297;
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                                                                                                                                                                   Score 365; DB 6;
Pred. No. 1.2e-30;
/ Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO16620 standard; protein; 1323 AA.
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                                                                                                                                                                         100.0%;
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27-JUL-2001, 2001JP-00227510.
28-SEP-2001, 2001JP-00302977.
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Matches 64, Conservative
                                                                                                                                                                                                                              64; Conservative
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                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 SQQC 376
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                                                                                                                     Seguence 1297 AA
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                                                                                                                                                                                                                                    Matches
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Gaps ö Length 1353;

Indels

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The invention computies the saints outd and coding sequence of a vortex invention will behavior described by the control of the invention one useful in the dispussion and treatment of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the invention of the inven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLEFM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and emppleasing therapy for, thrombocycopenic purpura, and for developing drugg for e.g. myocardial infarction and cerebral infarction.
                                                                                                                                                                                                                                                                                                                          Human von Willebrand factor (vWF)-cleaving enzyme-related protein #6
                                                                                                                                                                                                                                                                                                                                                                                            Human, protease inhibitor; gene therapy, wWP-leaving enzyme; von Willebrand factor-leaving enzyme; thrombocyropenic purpura; myocardial infarction; errebral infarction; arreficesits
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ilarity 100.0%; Pred. No. 1.2e-30;
Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamamoto T,
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                                                                          AAO16619 standard, protein; 1378 AA.
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27-JUL-2001; 2001JP-00227510.
28-SEP-2001; 2001JP-00302977.
25-JAN-2002; 2002JP-00017596.
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27-JUL-2001, 2001JP-00227510.
28-SEP-2001, 2001JP-00012977.
25-JAN-2002, 2002JP-00017596.
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Human ADAMTS-M polypeptide

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//note= "The mature form of the ADAMTS-M protein is processed by furin cleavage of the prodomain" 94...97 abel= Furin_cleavage_site Location/Qualifiers label= Prodomain leavage-site Key Peptide Protein

/label= Mature_ADAWTS-M_protein fnote= "The mature form of the ADAWTS-M protein is processed by furin cleavage of the prodomain"

label - Metalloprotease domain Domain Domain

10. 473 label= Thrombospondin submotif 19. .424 label= Heparin-binding_domain 47. ,272 label= Zinc-binding_motif .abel= Disintegrin_domain 394 nomain Domain Domain

099. .1156 label= Thrombospondin submotif

EP1152055-AL 07-NOV-2001

24-APR-2001, 2001EP-00303706 27-APR-2000: 2000US-0200040P

(PFIZ) PFIZER PROD INC

Walsh RT; Wachtmann TS, Mitchell PG, WPI; 2002-084275/12. N-PSDB; ABA02549. Buckbinder L.

New polymucieotide, useful in gene therapy, particularly for treating or preventing e.g. arthitis: croph's disease, Altheimer's disease and organ transplant coxicity and rejection, comprises ADAMTS polymucieotide and encoded polypeptide.

Claim 4; Fig 2; 31pp; English.

The present agentine represents a AAPNY process, designment AIANNTS M.

This contains the characteristics of the ADN in Designment AIANNTS M.

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410 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQASMCNTQACEKTQLEFM 469 1 WSSWGPRSPCSRSCGGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLEFM

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AAE24450 standard; protein; 1427 AA AAE24450;

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61 SQQC 64

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(first entry)

04-OCT-2002

Ruman, Von Willebrand factor-cleaving protease; vWF-cp) therapy, empyment therapy canadase, imminisation thrombomolic disease precedempsia, thrombotic introducytic purpura TTP; Repord School purpura thromboses; secretal thrombomy copeania, is seconjutic-ursemic applications, transpanic, auticologilatr; of/compones 9. Human Von Willebrand factor-cleaving protease (vWF-cp).

domo sabiens

note= "Mature human vWF-cp protein" "Furin cleavage site" note= "Catalytical side" label signal peptide Location/Qualifiers .228 mote= Cleavage-site Peptide Region

"Thromspondin type I motif" note= "Distintegrin like motif" "Cysteine rich region" note= "Met turn" .377 .439 553 note= note= tegion Domain

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated or substantially purified Von Willebrand factor-cleaving protease, useful for producing preparation for threapy of thrombosis and thromboembolic disease such as thrombotic thrombosits purpura.
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Conservative 0: Mismatches 0; Indels 0;
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                              /note» "Thromspondin type I motif"
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                                                                                                                                                                                                           20-NOV-2001; 2001WO-EP013391
                                                                                                                                                                                                                                                                   22-NOV-2000; 2000US-00721254
12-APR-2001; 2001US-00833328
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producing a purified human aggrecanase protein which can be used to
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100.0%; Pred. No. 1.3e-30;
iive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                       16-OCT-2001; 2001US-00978979
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                                                        Homo sapiens.
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WO200246383-A2

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08-DEC-2000; 2000US-0254399P. 52-DEC-2000; 2000US-0257603P. 05-DAN-2001; 2001US-0260110P. 19-JAN-2001; 2001US-026281P. 25-JAN-2001; 2001US-0264623P.

INCY-) INCYTE GENOMICS INC.

Azimzai Y, Kallick DA, Baughn WR, Griffin JA, Swarnakar A, Walla MK, Hafalia AAA, And-Young J, Blitott VS; r. J, Thengavell K, Lu Y, Warren BA, Lu DM, Lee EA; eg CM, Arvizu C, Delegene AM, Yao NG, Khan FA; Sanjanwala MM; Ramkumar J, Tribouley CM,

WPI; 2002-519664/55. N-PSDB; ABQ75946 New isolated Protein Modification and Maintenance polypeptides, useful for diagnosis, and treatment of e.g. gastrointestinal disorders.

Claim 1 (a); Page 154-157; 200pp; English

The invention that we to make the production may be used in the properties. Polypetides of the invention may be used in the adaposis, transment and presention of the production may be used in the adaposis, transment and present on of disperse sections of the production of the produ

Sequence 1445 Ah;

Indels 0, Gaps Onery Match 100.0%; Score 365; DB 5; Length 1445; Best Local Similarity 100.0%; Pred. No. 1.18-30. Sect Local Similarity 0.0.0%; Pred. No. 1.18-30. Indels 0.7 Wismatches 0; Indels 0.7 Wismatches 0.1 Indels 0.7 Wismatches 0.1 Indels 0.7 Wismatches 0.1 Indels 0.7 Wismatches 0.1 Indels 0.7 Wismatches 0.7 Wis Best Loca Matches

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61 SQQC 64

700 ADA50467 standard, protein, Human protease SEQ ID NO:65 (first entry) enzyme; human; protease. 20-NOV-2003 ADA50467;

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402003040393-A2 Homo sapiens. 15-MAY-2003.

04-NOV-2002, 2002WO-IB004615 06-NOV-2001; 2001US-0332633P DECO-) DECODE GENETICS EHF. Sigurdsson GT WPI: 2003-441582/41. Wartinez RAM,

N-PSDB; ADAS0514.

The invention misses to a coveni isolated polypoptic exceptings an amino and sequence that has greated than 39 is identity to any one of 47 isolated and any other contraction that has greated than 39 is identity to any one of 47 isolated by the contraction that is profess profess of any other and any other contraction that is profess of any other and any other any other and any other any other and any other and any other any other and any other any other and any other any other and any other any other and any other any other and any other any other and any other any other any other any other and any other any other and any other any other any other and any other any other any other and any other any other any other any other any other any other and any other any other any other any other any other any other any other and any other a Novel isolated protease polypepride and polymucleoride encoding the pypeptide useful for diagnosing and treating diseases or conditions associated with a protease. Claim 1, Page 71, 160pp, English.

Sequence 700 AA;

Gaps ö ch 12 Similarity 53.14; Score 206; DB 6; Length 700; 31 Similarity 53.14; Pred. No. 8.8e-14; 34; Conservative 10; Mismatches 20; Indels Local Similarity Query Match Matches

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RESULT 15 AAB85695

AAB85695 standard, protein; 1048 AA. (first entry) 29-OCT-2001 AAB85695;

Larynx carcinoma associated protein-1 (LarCAP-1) polypeptide

Larynx carcinoma associated protein-1; LarCAP-1; carcinoma; oyrostatic; antimetasiselic; antiarthritic; osteopathic; immunosuppressive; human; immunosimplatelimilari; cerebroprotective; vasciropic; antiinflammatory; watchie; demacological; oxidiant; vascire; 2525252555555

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Homo sapiens.
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WO200159133-Al.
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16-AUG-2001.

12-FEB-2001; 2001WO-SP001525, 14-FEB-2000; 2000EP-00102955.

(MERE) MERCK PATENT GMBH.

Duecker K, Hentsch B, Hoheisel J, Frohme M;

Laryux carcinos associated protein. Dolygaptide for the treatment of extroke, its carcinosas, metratesis, arthritis, oeregorosis, kimune disorders, ortroke, itehemia, autoimmune disease, angiogenesis, skin disorders and ortram malfunctions autoimmune disease, angiogenesis, skin disorders and WPI; 2001-483569/52. N-PSDB; AAH47048.

Claim 1; Page 33-39; 47pp; English.

This seprements a human introduction associated protection! LuczDa-1) polymptide. The largotal in LuczDa-1 polymptide in the largotal in LuczDa-1 polymptide in the secondarial exception are enclosible; the largotal topopeptide and polymptication are enclosible; the largotal polymptide in the polymptide are made as a faithfull, osteopropia, a immune disorders, errore, declear, and enclosured feet and indicated and organ maifunction especially heart hyperstophy.

Query Match 56.4%, Score 206, DB 4; Length 1048, Best Local Similarity 53.1%, Pred. No. 1.38-13, Maches 34, Conservative 10, Mismitches 20, Indels 0

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Sequence 1048 AA;

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61 SQQC 64

104 AQQC 407 ò

Search completed: March 13, 2004, 07:39:06 Job time : 10.3667 secs

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LENGTH: 365 amino acids TYPE: amino acid

SEGUENCE CHARACTERISTICS INFORMATION FOR SEQ ID NO: 5:

STRANDEDNESS: unknown

POPOLOGY: unknown

100.0%;

Local Similarity 100.

US-09-978-979-5

Query Match

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CURRENT APPLICATION NUMBER: US/10/222,334
CURRENT FILTEN DATE: JOSO-08-16
PRICHE PERCOR PERCORPORES: GOILS 394
PRICHE PERCORPORTS: JOSO-08-12,834
NUMBER OF SEQ. TO NOS: 78
SEQ. JD NOS: RESERVED TO NOS: 78
SEQ. JD NOS: A
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PRIOR APLICATION NUMBER: 60/312,834
PRIOR FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 78
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, Sequence 2, Application US/09836712
, Patent No. US20010049106A1
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J ORGANISM: Homo sapiens

US-10-222-334-4
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US-09-836-712-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 1416
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APPLICANT: Lowy, Callia
APPLICANT: Low, Callia
TITES OF STRUKTHIS, DAVIS, Genes and Proteins and Variants, and Daes Thereof
TITES OF STRUKTHIS, UN-07288
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                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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LOCATION: (365)..(365)
OTHER INFORMATION: unknown amino acid
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NAME/KEY: MISC_FEATURE CTHER INFORMATION: unknown amino acid

FEATURE: FEATURE:

113-10-057-487-5

ORGANISM: homo sapiens

TYPE: PRI

NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin version 3.1 SEQ ID NO 5 LENGTH: 365

Sequence 5, Application US/10057487 Publication No. US20030105313A1 GENERAL INFORMATION:

JS-10-057-487-5

119 SQQC 122

61 SQQC 64

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Sequence 4, Application US/10223334 Publication No. US20030073116A1 GENERAL INFORMATION:

US-10-222-334-4

119 SOOC 122

61 SQQC 64

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SEQ ID NO 2 LENGTH: 1427

Best Loca Matches

ò 8 US-10-057-487-8

, ORGANISM: Homo sapiens US-10-014-070-5

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PRIOR APPLICATION NUMBER: 60/212,336; 60/213,955; 60/215,396; 60/215,821; 60/218,944

THE FILMS PRIME OFFER: 2000-06-16; 2000-06-22; 2000-06-29; 2000-07-07; 2000-07-14

NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                          488 WSSWIKEGSCSRSCGGGVRSRSRSCNNPSPAYGGRPCLGPMFEYQVCNSEECPGIYEDFR 547
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1. Similarity 55.1%; Pred. No. 2.7e-14;
1. Similarity 53.1%; Pred. No. 2.7e-14;
1. Conservative 1.; Mismatches 5., Indels 0.
                    Ouery March 56.4%, Score 206; DB 13; Length 1156; Bet Local Similarity 53.1%; Pred. No. 26e-14; Marches 34; Conservative 10; Pred. Rectees 20; Indels 0
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OTHER INFORMATION: Incyte ID No. US20040023243A1 7477386CD1
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CURRENT APPLICATION NUMBER: US/10/311,035
                                                                                                                                                                                                                                                                                                                                                                            US-10-311-035-10
; Sequence 10, Application US/10311035
; Publication N. US20040023243A1
; GENERAL INFORMATION:
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AU-YOUNG, Janice
TRIBCULEY, Catherine M.
DELEGEANE, Angelo M.
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RAMKUMAR, Jayalaximi
XU, Yuming
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APPLICANT: YUE, Henry
APPLICANT: ELLIOTT, VICK!
APPLICANT: GANDHI, Ameena R.
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CHAWLA, Narinder K.
YAO, Monique G.
LU, Dyung Aina M.
ARVIZU, Chandra S.
TANG, Y. Tom
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NGUYEN, Danniel B.
LEE, Ernestins A.
HAFALIA. April
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APPLICANT: KEARNEY, Liam
APPLICANT: KALLICK, Deborah A.
TITLE OF INVENTION: Protesses
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Best Local Similarity
Matches 34: Conserve
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                                                                                                                                                                                                                            61 SQQC 64
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LENGTH: 1189
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18-7 WSWGTRSPCSRSCGGGGUVTRRRCCNNPRPAFGGRACUGADLOADMCNTOACKTOLEFM 446
                                                                                                                                                                                                                                                 387 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEXTQLEFM 446
                                                                                                                                                                                                   1 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLEFM 60
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100.0%; Pred. No. 1e-31;
tive 0; Mismatches 0; Indels 0;
                                                                                            th 100.04; Score 365; DB 14; Length 1427; [Similarity 100.04; Pred, No. 18-31; Chidels 0; GA, Conservative 0; Mismatches 0; Indels 0;
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APPLICANT, CARTIS, ROOY A.J.
APPLICANT, CARTIS, ROOY A.J.
APPLICANT, MILIORIUM PRARMOCHILIS, INC.
APPLICANT, MILIORIUM PRARMOCHILIS, INC.
TITLE OF INVESTOR'S 55014, A Human Meet alporteese Family
TITLE OF INVESTOR'S 65014, A Human Meet Therefor
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THIE REFRENCE: 0870.2.03 MINER: US/10/057,487
CURRENT FILMS TOWN: 2002-01-25
CURRENT FILMS TOWN: 2002-01-25
BRIGH APPLICATION NUMBER: 60/421,469
PRIGH APPLICATION NUMBER: 60/421,469
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CURRENT APPLICATION UNDER: US/10/014,070
CURRENT PILLNG DATE: 200-11-13
PRIOR APPLICATION WHOREX: 60/258,373
PRIOR FILING DATE: 2000-12-22
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1156
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Publication No. US20020119555A1
GENERAL INFORMATION:
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Publication No. US20030105313A1
GENERAL INPORMATION:
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LENGTH: 1427
TYPE: PRT
ORGANISM: homo sapiens
7 TYPE: PRT
7 ORGANISM: Homo sapiens
US-10-222-334-2
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Best Local Similarity
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US-10-057-487-8

Query Match

Matches

0-014-070-5

TYPE: PRT

Sequence 14, Application US/09938330 Patent No. US20020115838A1 GENERAL INFORMATION:

US-09-938-330-14

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Best Local Similarity 53.1%; Pred, No. 2.8e-14; Macches 34; Conservative 10; Mismatches 20; Indels
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PRIOR PLING VATE 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR PLING DATE: 2000-09-19
NUMBER OF SEQ ID NGS: 26
SOTTAME: PRESEQ for Mindows Version 4.0
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Patent No. US20020115838A1
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Turner, C. Alexander Jr
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APPLICANT: Scoville, John
APPLICANT: Friddle, Carl Johan
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US-09-938-330-10
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Query Match
Se.44; Score 206; DB 9; Length 1213;
Best Local Similarity 53.18; Pred. No. 28e-14.
Matches 34; Conservative 10; Mismatches 20; Indels '

ORGANISM: homo sapiens

TYPE: PRT

SOFIMALE. SEQ ID NO 14 US-09-938-330-14 56.4%; Score 206; DB 9; Length 1216;

, ORGANISM: homo sapiens US-09-938-330-12

Query Matc)

LENGTH: 1222

SEQ ID NO 8

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1 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLEFM 60
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Job time : 5.06667 secs
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Patent No. US20020115838A1
GENERAL INFORMATION:
                                                                                                                                  ) ORGANISM: Homo sapiens
US-10-205-368-4
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ORGANISM: homo sapiens
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SEQ ID NO 4
LENGTH: 1223
TYPE: PRT
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LENGTH: 1232
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Local Similarity 56.4%; Score 206; DB 13; Length 1223;
Local Similarity 53.1%; Pred; No. 2.8e.14
Local Similarity 09.00 Nismarches 20; Indels 0
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Gert Local Similarity 53.1%; Pred. No. 2.8e-14.

Matches 34; Conservative 10; Mismatches 20; Indels (
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POBLICATION PROPERTION TO A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PAGILSTEIN BILL STRONG A PA
                                                                                                    TYPE: PRT
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US-10-014-070-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        615 AQQC 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              515 AOOC 618
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US-10-205-368-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Si
Matches 34;
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Sequence 12, Appl

60 1 US-07-646-531D-12

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146 28

GenCore version 5.1.6	0.0
Copyright (c) 1993 - 2004 Compugen Ltd.	39,9 469 1 US-08-313-288B-15 Sequence 15
OM protein - protein search, using sw model	441 3 US-08-985-526-3 Sequence 3, 859 4 US-09-364A-5 Sequence 5, 873 775-09-906-48-5 Sequence 5,
Run on: March 13, 2004, 07:34:04 ; Search time 2.7 Seconds (Without Signments) (Without tilg ments) 123:777 (13:777 till updates/sec	134 36.7 943 1 105.95-106.9928.7 Sequence 7. 131 35. 36. 135. 3 105.95-95.958.7 Sequence 7. 131 35. 3 105.95-95.95 305.95
Title: US-09-836-712-2_COPY_410_473 WS:WGPRAPCBRCGAGGYTVTEXCNTQACEXTQLEPWSQOC 64	35.6 1156 3 US-09-423-546-1 35.1 218 3 US-08-985-526-1 34.8 262 4 US-08-800-729-125
Scoring table: BLOSUM62 Gapop 10:0 , Gapoxt 0.5	127 3 4.8 175 4 05-03-00-07-29-09 126.5 34.7 59 4 08-09-197-770B-18 125 34.2 699 2 08-09-197-770B-18 125 24.2 699 2 18-09-18-5
Searched: 389414 seqs, 51625971 residues	
Total number of hits satisfying chosen parameters: 389414	ALIGNMENTS
Minimum DB seq length: 0 Maximum DB seq length: 2000000000	RESULT 1
Post-procesing: Minimum Match Ot Maximum MaxCh 1004 Maximum Street S summaries	Sequence 4, Application US/09930872 Sequence 4, Application US/09930872 Factor No. 1985 Sequence 1
Decabase : Ilemed Parents AA, 14, COMB.pp. : 1. / Copi. 6, prodet.//isal.sp. : 2. / Copi. 6, prodet.//isal.sp. : 2. / Copi. 6, prodet.//isal.sp. : 2. / Copi. 6, prodet.//isal.sp. : 2. / Copi. 6, prodet.//isal.sp. : 2. / Copi. 6, prodet.//isal.sp. : 3. / Copi. 6, prodet.//isal.sp. : 6. / Copi. 6, prodet.//isal.s	APPLICANT, Hillian, Erry, Hillian, Erry, Hillian, Erry, Hillian, Erry, No. 444838881 human Protesses and Polymucleotides Encoding the ITTHE REPRESENTS INT. ACTUAL NO. 1979.00 pt. 97. CTRESENT FILLIAN ACTUAL NO. 1979.00 pt. 97. CTRESENT FILLIAN ACTUAL NO. 1979.00 pt. 97. PRICA PARLOCHTON WIRESENT SOLICI-SEL NG 607.255.852 NUTRIES FILLIAN ACTUAL NO. 1979.00 pt. 97. PRICA PARLOCHTON WIRESENT SOLICI-SEL NG 607.255.852
Pred. No. is the number of results predicted by chance to have a scree greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SOFTWARD 4 SEASON for Mindows Version 4.0 SED THE STATE THE SEC IN MINDOWS VERSION 4.0 SED THE STATE THE SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC
SUMMARIES) Tibe: FKI) OKGANISM: home sapiens IS. no. 930-830-82-4
Result Query No. Score Match Length DB ID Description	Query Match 52.6k; Score 192; DB 4; Length 1224;
1 192 52.6 1224 4 US-09-930-872-4 Sequence 4, Appli	BESC LOCAL SIMILARILY 45.3%; Fred. No. 9.78-12.) Matches 30, Conservative 12, Mismatches 22, Indels 0, Gaps 0;
50.1 1205 4 US-09-491-522-11 49.0 874 4 US-09-3691-523-11 40.0 874 4 US-09-369-3644-15	Qy 1 WSSWOPRSPCSRSCQGOVTRRRQCNNPRPAFGGRACVGADLQAEMCXTQACERTQLEFW 60 The same wschwesksep-cyclogovyessaltcyneydsiggartcygdyrghacytchygologovyeria
177 48.5 1211 4 US-09-491-522-5 Sequence 5, 177 48.5 1211 4 US-09-491-522-5 Sequence 9, 175 47.9 905 4 US-09-36-364A-9 Sequence 9, 175 47.9 905 4 US-09-36	
163 44.7 105.1 US-08-313-288B-19	Db 649 AAQC 652
161 44.1 930 4 US-09-364.8-2 Sequence 2, 161 44.1 1170 1 US-08-313-288B-20 Sequence 20 157 43.0 239 5 PCT-US93-01652-1 Sequence 1.	RESULT 2 US-09-369-364A-13
155.5 42.6 551 4 U8-09-130-491-16 Sequence 16, 155.5 42.6 608 4 U8-09-1491-13 Sequence 13, 155.5 42.6 72.7 72 10-10-448-0732.	<pre>; Sequence 11, Application US/09369364A</pre>
155.5 42.6 72.7 4 US-02-48-023A-12 Sequence 12, 155.5 42.6 949 4 US-09-445-023A-12 Sequence 12, 155.5 42.6 949 4 US-09-568-559-2 Sequence 2.	, APPLICANT: Apre. Suneel; APPLICANT: Hurskainen, Tiina L.
155.5 42.6 967 4 US-09-130-491-2 Sequence 2, 154.5 42.3 757 4 US-09-963-791-24 Sequence 24,	; APPLICANT: Hirohata, Satoshi ; TITLE OF HYRWITUP: Nucleic Acids Encoding Zinc Metalloproteases
154.5 42.3 908 4 US-09-562-1286A-2 Sequence 2, Al 154.5 42.3 908 4 US-09-653-791-2 Sequence 2, Al	CURRENT APPLICATION NUMBER: US/09/369,364A CURRENT PILIN DATE: 1999-08-06
24 153 41.9 518 4 105-09-162-5644-22 Sequence 22, Appl 25 153 41.9 930 4 105-09-122-1268-15 Sequence 15, Appl 26 153 41.9 930 4 105-09-634-2868-15 Sequence 15, Appl	; NOWHARE OF EXT ID NOS: 51 ; SEQ ID NO 13 ; SEQ ID NO 13
150.5 41.2 2165 4 US-09-800-729-155	, LENGTH: 1882

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121 WGPWGPWGQCSRTCGOOIQPSNRECDNPAPQNGGRPCLGBRVKYGSCKTBECPPNGKSFR 180
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                                                             558 WGAWSPEGSCRITCGTGVKFRTRQCDNPHPANGGRICSGLAYDFQLCNSQDCPDALADFR 617
1 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLEFM 60
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**TILLE OF STREETING (ANGEST D. TANGO.71, TANGO.74, TANGO.76, AND TANGO.91

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APPLICANT: Hirskeinen, Thina L.
APPLICANT: Hirobatea, Satoshi
THIE OF INVENTIOR: Muchica, Acids Encoding Jinc Metalloproteases
FILE REPERBAUER: 26473/4007/10-30-00
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43.8%; Pred. No. 1e-11;
tive 9; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query March 49.0%; Score 179; DB 4; Length 874; Beset Local Similarity -43.8%; Pred. No. 1.1e-11. Mechies Ps. Conservative 11; Mismarches 25; Indels Metches 28; Conservative 11; Mismarches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILIND DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PREENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                      , Sequence 15, Application US/09369364A
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Patent No. 6416974
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Mus musculus ADAMTS-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 43.8
Matches 28; Conservative
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                                                                                                                                                                                                                              518 BBQC 621
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                                                                                                                                                 61 SOOC 64
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                                                                                                                                                                                                                                                                                                                                         RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLBFM 60
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                                                                                                                                                                                                                                                                                                                                                                       Query Match Length 1882;
Baet Local Similarity 6:34; Pred No. 1.18-1. Local Similarity 6:34; Pred No. 1.18-1. Analogue 0; Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APRICANT: OLIGHE, ALABARAN PRECIONEL LEGEN CONTROL OF A PRECIONEL LEGEN CONTROL CONTROL OF A PRECIONEL PROPERTY PROPERTY ON THILD OF INVESTION IS RECOGNISMENT W-PROTEINARS.
THILD OF INVESTION IS AROTHER PRODUCTION, METHODS AND USSS THERROF WINNERS OF SEQUENCES: 17
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50.1%; Score 183; DB 4; Length 1205;
Best Local Similarity 46.9%; Pred. No. 5.4e-12.
Marches 30; Conservative 8; Mismatches 26; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows
SOFTWARE: FeasERD for Windows Version 2.05
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8389-0060-999
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ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/09491522
Patent No. 6428998
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE:
ATYCKNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGIGTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
       ORGANISM: Homo sapiens ADAMTS-9
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELERAK: 650-493-556
TELERAK: 650-493-556
TELERAK: 650-493-556
TELERAK: 650-41 PRINTE
SEQUENCE CHARACTERISTICS:
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                                                                                                                  LOCATION: (468)

OTHER INFORMATION: Xaa = C
NAME/KEY: MOD RES
                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa = Y
US-09-369-364A-13
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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                                                                                    NAME/KEY: MOD RES
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                                                                                                                                                                                                                                     LOCATION: (521)
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US-09-491-522-11
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545 WGPWRPWGCSRICGGGIQFSNRECDNPMPQNGGRPCLGERVKYGSCNIEECPPNGKSFR 604
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MARCHANNIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCHANIA MARCH
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                                                                                                                                                                                                                                                                                                                                                                                                                            45.2%; Score 165; DB 4; Length 1081;
42.2%; Pred. No. 4.5e-10;
tive 8; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 47.9%; Score 175; DB 4; Length 905; Best Local Stailarity 43.8%; Fred. No. 3.1e-1. Indels Matches 28; Conservative 9; Mismatches 27; Indels
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Patent No. 6391610
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09369364A
Patent No. 6391610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mus musculus ADAMIS-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 42.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           605 BQQC 608
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US-09-369-364A-7
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98.54; Score 177; DB 4; Length 1211;
Best Local Similarity 45.34; Pred. No. 2.5e-11,
Matches 29; Conservative 9; Mismatches 26; Indels
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New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09369364A
Patent No. 6391610
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Abrams, Samuel B
REGIGTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 836
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                 181 EQQC 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-09-491-522-5
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SENERAL INFORMATION

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541 WSGWSAWSICSRSCGMGVQSAERQCTQPTPKYKGRYCVGERKRFRLCNLQACPAGRPSFR 600
                                                                                                                                                                                            1 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPAFGGRACVGADLQAEMCNTQACEKTQLEFM 60
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                                                                                      44.7%; Score 163; DB 4; Length 997;
ilarity 46.9%; Pred. No. 6.9e-10;
Conservative 5; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: JOSEPH THOMS M. and AVIDE KLAR APPLICANT: JOSEPH TOWNING, KERESSICH AND USES OF A TITLE OF INVESTION: CLOKEN, KERESSICH AND USES OF A TITLE OF INVESTION: NOVEL SECRETED PROTEIN, P-SEPONDIN CHARGE OF SERVENCES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINA TYPE: Plogpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOTTANGE: PREMETIN Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: White, O'thip P.
REGISTRATION NUMBER: 28.679
REFERENCY DOCKET NUMBER: 40038-A-PCT-US
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATIONS: (212) 231-05-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/0831328BB
Patent No. 5750502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-369-369-364A-2
; Sequence 2, Application US/09369364A
; Patent No. 6391610
               , ORGANISM: Homo sapiens ADAMIS-7
US-09-369-3648-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1172 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                Query Match
Best Local Similarity
Matches 30; Conserva
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STATE: New York
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TYPE: PRT
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570 WGSWGPWGQCSRSCGGGVQFAYRHCNNPAPRNSGRYCTGKRAIYRSCSVTPCPPNGKSFR 629
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APPLICANT: Age immed.
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1 Similarity 45.3%; Pred. No. 1.1e-09;
29; Conservative 2; Mismatches 33; Indels
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CURRENT APPLICATION DATA
PAPLICATION NUMBER: US/08/313,2888
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TELECOMNILOGINICOMNATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET OWNERS THE STREET OWNERS THE STREET OWNERS THE STREET OWNERS THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK THE NEW YORK TH
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5750502
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FILING DATE: January 5, 1995
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REGISTRATION NUMBER: 28,678
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US-09-369-364A-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 1170 amino acid
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MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy
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Best Local Similarity
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GENERAL INFORMATION:
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SEQ ID NO 2
LENGTH: 930
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44.1%; Score 161; DB 1; Length 1170; 51.9%; Pred. No. 1.3e-09;

Query Match Best Local Similarity

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Seguence, i.g., Application US/09110491
Patent No. 6446574
APRICATION SOLIENAL DOGSLER A.
APPLICATION SOLIENAL DOGSLER A.
APPLICATION SOLIENAL DOGSLER A.
TITLE OF INVENTION FANCE-71, TANCE-74, TANCE-75, AND TANCE-83
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0; Gaps
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                                                                                  495 WGPWSPWDICSVTCGGGVQKRSRLCNNPTPQFGGKDCVGDVTENQICNKQDC 546
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                                      1 WSSWGPRSPCSRSCGGGVVTRRRQCNNPRPARGGRACVGADLQAEMCNTQAC 52
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Pred. No. 7.7e-10;
4; Mismatches 21; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UPSEALTING SYSTEM; PC-705/NS-708
SOFTWARE ARentlin Release #1.0, Version #1.25
CRREAT AFECTATION DATA
FLIND BORNER NEWS PCT/USS3/01652
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STREET: 100 South Wacker Drive, Suite 960
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FILLNG APPLICATION DARN:
APPLICATION NAMES: US/07/464,369
FILLNG DART: 12-78A-1997/464,369
APTONEN'S ARRAY INFORMATION:
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REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: 92005-PCT
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COUNTRY: USA
ZIP: 60606-4002
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
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Best Local Similarity 51.9%;
Matches 27; Conservative 4
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TELEPRA: (312)-456-7776
INFORMATION FOR SEQ ID NO. 1: SEQUENCE CHARACTERISTICS:
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, MOLECULE TYPE: peptide
PCT-US93-01652-1
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CORRESPONDENCE ADDRESS:
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US-09-130-491-16
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STATE:
Matches
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Pred. No. 2.5e-09;
9; Mismatches 28; Indels 1;
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42.6%; Score 155.5; DB 4; Length 609;

Beet Local Similarity 41.5%; Pred. No. 2.8e-09;

Matches 27; Conservative 9; Mismatches 28; Indels 1:
TILE REPUBLICATION UNDERS. 105 (1971) 491
CURRENT APPLICATION UNDERS. 105 (1971) 491
CURRENT TILE DATE, 1982 105 (1981) 105
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Job time: 2.7 secs
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Patent No. 6416974
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Matches 27; Conservative
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ORGANISM: Rattus rattus
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US-09-130-491-13
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A; Reference number: 219413
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score greater than or equal to the score of the result baing printed,
and its derived by analysis of the cotal score distribution.
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                                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: GB:chr_V, PIDN:AAC25867.1; PID:g3294501; GSPDB:GN00023; CESP:C37C3
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A.Rogarimental sources strain Bristol N2; clone C37C3
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A) Abmaidene : 1.1559, SRF - GG2>
A) CTOBE-REFERENCE REMILLER (SESPICATION FOR CASE OF LICENSE (SESPICATION FOR CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE OF CASE O
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C.Speciaen Caenothabdetis elegams envision 15-Oct-1999 #text_change 18-Peb-2000
C.Dete: 15-Oct-1899 #feequae_grvision 15-Oct-1999 #text_change 18-Peb-2000
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Species: Caenorhabditis elegans
C) Bate: 22-000-1599 Resquance_revision 29-0ct-1999 #text_change 01-Dec-2000
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submitted to the RMEL bata Library, July 1996
submitted to the RMEL bata Co. elagans cosmid C37C3
sylpsecription: The sequence of C. elagans cosmid C37C3
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Pred. No. 0.0079;
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A,Molecule type: DNA
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ilarity 34.5%;
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Matches 19; Conserva
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Best Local Similarity
Matches 19; Conserve
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A,Status: preliminary
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A,Residues: 1-1558 <
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A,Gene: CBSP:F25HB.3
A,NBQ Požítzon:
A,Tatropone: 31/1: 52/1: 135/2: 133/3: 216/1: 266/1: 495/2: 547/3: 584/3: 534/2: 744/1: 81
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Keywords: hydroises, metalloproteinase
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Algencia Peciliniary; translated from GB/DMBL/DDBJ
Algenciane: 1-1595 4MIL.
Algenciane: Elegancia EMBL/SBJSBS
Algencianeia, source: colone 57386
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submitted to the EMBL Data Library, February 1996
A.Daestrpfon; Cloning of the CNA of the bovine procollagen I N-proteinase.
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Cobes: Caenothabditis elegans
Cobes: 12-Ccr. 1999 Heaquence_revision 15-Oct. 1999 Htax._change 15-Oct. 1999
Cobes: 10-Ccr. 1999 Heaquence_revision 15-Oct. 1999
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Pickernet names procollagen P-proteinale
Cisperse: Bos printganiue taurus (catrille
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AixCoseimencel Govices (Bin)
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Pred. No. 0.0011;
6; Nismatches 23; Indels 5;
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Pred. No. 0.001,
7; Nismatches 21; Indels 9;
                                                                                                                                                                                              Score 112, DB 2, Length 2165,
Pred. No. 0.00012,
6; Mismatches 26, Indels
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A.Reference number: 219578
A.Accession: T22545
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Best Local Similarity 38.2%;
Matches 21; Conservative
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Best Local Similarity 33.94
Matches 19, Conservative
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A; Accession: T18517
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Best Local Similarity
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R/Cottage, A. submitted to the EMBL Data Library, November 1995

Query Match 26.9%; Score 93; DB 2; Length 788; Sest Local Similarity 41.8%; Fred, 700.0.0072. Metables 22; Conservative 4; Mismatches 15; Indels Matches 22; Conservative 4; Mismatches 15; Indels

A; Introns: 20/1; 47/1; 76/1; 152/1; 735/2; 754/2

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C;Species: Gallus gallus (chkicken)
C;Dates: 10-68pe: 1999 Henguence_revision 10-8ep-1999 #text_change 10-Sep-1999
C;Accession: A39804
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Pred. No. 0.026;
3; Mismatches 11; Indels 23; Gaps
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Pred. No. 0.0077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ritawler, J.; Duquette, M.; Ferro, P.
J. Biol. Chem. 266, 8039-8043, 193.
A.Title: Cloning and sequencing of chicken thrombospondin.
A.Reference number: A39004, MOID:91217056; PMID:2022631
                                                                                                             ilarity 40.0%; Pred. No. 0.007
Conservative 2; Mismatches
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20; Conservative
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R.Kuno, L. Lassa, H.; Ohno, S.; Matamahima, K.
Artucis 46, 46471, 13997 Copmitted for Committee of Activity Copmittee of Activity Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee of Committee 
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A.Experimental source: strain 1295VJ
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Cigneries Mus matenius (house mouse)
Cibate: 22-dai-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
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C:Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                 1 WHVGTWMECSVSCGDGIQRRRDTCLGPQAQAPVPADFCQHLPKPVTVRGCWAGPC 55
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A:Introme: 228/1, 343/3; 388/1; 444/1; 539/3; 602/1; 660/3; 719/2
(S:Sperfamily: thrombospondin type 1 repeat homology
F:542-598/Domain: thrombospondin type 1 repeat homology <THR3>
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A.Reference number: 214055; MUID:98110583; PMID:9441751

A,Status: preliminary, translated from GB/EMBL/DDBJ A,Molecule type: DNA

A.Residues: 1-951 <KUN>

Genetics:

ch 1. Similarity 38.2*; Pred. No. 0.0097, 21. Conservative 3; Mismatches 28; Indels

Local Similarity

Query Match Sest Local Si Matches 21

Lenath 550;

DB 2;

26.4%; Score 91.5;

A;Note: DKFZp762C1110.1

Query Match

A.Accession: T47158
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-550 cAAA
A.Cross-references: EMBL:AL162080

Ouery Match 25.7%; Score 89; DB 1; Length 1178; Best Local Shallarity 33.9%; Pred. No. 0.03; No. Matches Askitches 24; Indels Matches 19; Conservative 7; Mismatches 24; Indels

A.Description: The sequence of C. elegans cosmid T19D2. A;Reference number: Z18599

A.Accession: T1692 A.KStatus: preliminary; translated from GB/SMBL/DDBJ A.Molecule type: DNA

A; Residues: 1-860 <BEN>

36.0%; 18; Conservative

Query Match Best Local Similarity

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1713.1816, 957, 881.710.106/Nainting stre: carbohydrate (Asn) (covalent) fetatus pre-
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1866, 2910/josalfish bonds: spraum predictor arbohydrate (Asn)
                                                                                     C, Geoceanin (1908) (M. M. M. Wayline, M. J. Tanaka, A. J. Kotani, H. J. Womura, N. J. Ohara, o. DNA Res. S. 3.139, 1384.

NA Release (M. S. 139) (1908) (M. M. M. Wayline, M. J. Tanaka, M. J. Kotani, H. J. Wanningenes, T. Tana Compliana, T. A. Reference number: 130, 13186 (MID: 92230154) (MID: 9523054)
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A/Roberduse is PRESIDENT (PRESIDENT) NID:GBJG4733; PIDN:BAA25531.1; PID:GBJG4734
A/Crose-deferonces ROBE.ARG11177; NID:GBJG4733; PIDN:BAA25531.1; PID:GBJG4734
C;Date: 01-Peb-1999 #sequence_revision 01-Peb-1999 #text_change 21-Jul-2000
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A.Dertimental source: fibrollat
A.Note: sequence extracted from NCBI backbone (NCBIN:95091, NCBIP:95096)
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A;Map position: 6927-6927
C;Complex: homotrimer, disulfide linked
C;Function:
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A,Residues: 560-1172 <LA2>
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A,Note: KIAA0605
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A,Introns: 56/3; 96/1; 171/3; 199/3; 245/2; 293/2; 335/3; 395/3; 426/3; 484/2; 505/3; 58
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A;Introne: 9/1; 34/3; 57/1; 90/3; 128/3; 162/1; 205/1; 285/2; 417/1; 475/1; 606/1; 745/
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C.Species Caenorhabditis elegans
C.Species (2-0-0-1399 Resquence_tevision 29-0ct-1999 #text_change 29-0ct-1999
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                                                                                                                                                                                           6; Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       774 WSDCSVNCGEGVOFRKRACF-----AAFCR-GKDSDVRNCYGGRC 812
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Pred. No. 0.026;
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7,612/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

hypothetical protein KIAA0605 - human C;Species: Homo sapiens (man)

RESULT 14 T00260

Match 24.9%; Score 86; DB 2; Length 805; Local Similarity 29.4%; Pred. No. 0.046; S. Indele 20; Conservative 7; Mismatches 25; Indele

Query Match Best Local Si Matches 20;

A;Status: preliminary, translated from GB/BMBL/DDBJ A;NOSicuse type: DNA A;NEsiducis: 1-805 -804 A;Eresiducis: 1-805 -804 A;Cross-references: EMBL:U41264, PIDN:AAA82427.1, CESP:F10E7.4

R.Penicky, A. Sabnitary, N. Sabnitary, November 1995 Sabnitted to the EMBL Data Library, November 1995 A.Description: The sequence of C. elegans commid Pl027. A.Reference number: 221489

C,Accession: T34212

Cuery Match 23.84; Score 82.5; DB 1; Length 1172; Best Local Smilarity 46.94; Pred No. 0.17. Matches 15; Conservative 4; Mismatches 6; Indels 7; Gaps

Search completed: March 13, 2004, 07:44:39 Job time: 2.02396 secs

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141681 segs, 52070155 residues Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table: Searched:

Fotal number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

141681

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result baing printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match J	Length	DB	QI	Description
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-	123.5		1906	н	AT20_MOUSE	mus m
61		35.1	1081	Н	AT18 HUMAN	homo
9			1935	н	ATS9 HUMAN	homo
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9			1211	-	ATS2 HUMAN	h ad
4	104.5		1205	н	ATS3_HUMAN	Ol5072 homo sapien
89			1205	н	ATS2 BOVIN	p ada
on.			908	н	ATS8_MOUSE	mus m
10			890	H	ATS8 HUMAN	cmod
11		28.5	1593	н	AT12 HUMAN	nomo.
12	86		1210	-	AT19 MOUSE	P59509 mus musculu
13				н	AT15_MOUSE	
14	95.5		1213	н	ATS2_MOUSE	QBc9w3 m adamts-2
15	÷	27.3	1223	н	AT14 HUMAN	homo
16			1224	-	AT16_HUMAN	homo
17		26.9	1207	-	AT19 HUMAN	pomod
18	92.5		967	-	ATS1 RAT	rattr
19		26.7	968	-	ATS1_MOUSE	
20			1173	et	TSP1_XENLA	xeno
21	91.5		967	-1	ATS1 HUMAN	Oguhi8 homo sapien
22		25.9	17	-	TSP2_MOUSE	mus c
53	83		1178	-	TSP2_CHICK	gallu
24			1095	-	AT17_HUMAN	pomod :
52	86.5		9	-	ATIO HUMAN	homo
56		25.0	1170	e	TSP2_BOVIN	DO8
27	85		525	-	ATL1 HUMAN	homo
28			450	П	AT10 MOUSE	mus m
53	82.5		1172	Н	TSP2_HUMAN	рошо
30		ė	1572	Н	BAI2 HUMAN	O60241 homo sapien
31	81		13	Н		3178 bos
32		ë	1170	Н		5441 mus m
33	80.5		1093	н	SMSB_HUMAN	Q9p283 homo sapien

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DISINTEGRIN-LIKE.
TSP TYPE-1 1.
CYS-RICH. 159 178 1. 15 1. 1 EMBL, AJ512753, CAD54808.3; -. EMBL, AY189815; AAC74895.1; -. EMBL, AY189816; AAC74896.1; -. MGD, MGI.2660628; Adamses0. 212041 Ž 250 250 465 609 721 843 906 1017 1426 CARBOHYD ACT SITE METAL CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD ARSPLIC VARSPLIC CONFLICT CONFLICT DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN METAL METAL

DB 1; Length 1906;

Score 123.5;

35.7%;

Query Match

1 WHVGTWMECSVSCGDGIQRRRDICLGPQAQAPVPADFCQHLPKPVTVRGCWAGPC 55 Best Local Similarity 40.0%; Pred. No. 2.6e-06; Matches 22; Conservative 8; Mismatches 24; Indels

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10-0CT-2013 [Rel. 42, L 1416 WYRGPWKSCSASCGKGVKYREVLCI-DOPORKLEEKYCSHLHKPRTHKACRSGRC 1469 PRODURED REAN INDREALIBERILE, GREADY, CARDAY C., Quesda V., MODINEAL SERVICE, CARDAY A., Limanares V., Carday C., Conseada V., Carday C., Carday A., Carday C., Carda Bikaryota Metazoa Chordata; Cranista, Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Cararthini; Hominidae; Homo. PRT; 1081 AM EMBL; AJ311903; CAC83612.1; -. Genew; HGNC:17110; ADAMTS18. STANDARD: Homo sapiens (Human). AT18 HUMAN QBTE60; ADAMTS18.

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24; Indels 1; Gaps
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N-LINKED (GLCNAC...) (POTENTIAL)
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9; Mismatches 24
        BY SIMILARITY.
ADAMTS-18.
METALLOPROTEASE.
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(9928) (9929) (9 Homo sapiens (Human)

Rukaryota, Merazoa; Chordata, Craniata, Vertebrata, Eureleostomi; Mammalia; Euriheita, Primares; Catarrhini; Hominidae; Homo. NCBL_TRATI=9606; Clark M.E., Kelner G.S., Turbeville L.A., Boyer A., Arden K.A., Maki R.A., MEDLINE=20396138; PubMed=10936055; SEQUENCE FROM N.A. (ISOFORM 3). TISSUE=Fetal

ADAMTS 9, a novel member of the ADAM-TS/Metallospondin gene Genomics 67:343-350(2000). Eamily Family

MEDINESTIRIPES, BENDESTIRISE, REDESTIRISE N. M. UNIGER K. A., Engle J. M., Rose M. Romerville R. P., Longure J. M., Unigers K. A., Engle J. M., Rose B., Towards C., Might T. M., "delote R., Pape S. S., "Chastockerization of JADWINS-9 and JADWINS-20 as a distinct JADWIN subfamily stated to Centerchabditis Global Comp. T. J. Blod. (Des. 278:9503-9513 (2003). SEQUENCE FROM N.A. (ISOFORM 1), AND FUNCTION.

SEQUENCE OF 159-1935 FROM N.A. (ISOFORM 2) TISSUE=Brain;

WEDLINESORIES, Explored-prisses, Wigness-T., Kituno R., Chare O.; Prédiction of the coding sequences of unidentifiéd human genes. XVI. Prédiction of the coding sequences of unidentifiéd human genes. XVI. The complete sequences of 150 me CDNA clones from brain which code Cot large proceins in vitro.", in VITRO." IN The COMP. The CDNA CLOSE SEQUENCES OF THE COMP. TH

and version.

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Name of Policy 13, 1990 | Name of Section 2) | Name of Section 2, Name

-i- SIMILARITY: Belongs to peptidase family M12B.
-i- SIMILARITY: Contains d idantegrin-like domain.
-i- SIMILARITY: Contains 1 GON domain.
-i- SIMILARITY: Contains 15 TSP type-1 domains.

This assistance marry is copyright, it is produced through a Colliboration between the Soiss Institute of Sichiforation and the REGI, outration, the burgean inclinionalist Institute. There are no restrictions on its being and soil of the statement of the statem EMBL; AF261918; AAF89106.1; -. BMBL; AF488803; AAO15765.1; -. BMBL; AB037733; BAA92550.1; -. HSSF; P15.67; AAT.

Senew: HGNC:13202: ADAMTS9. MEROPS; M12.021; 605421,

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PROJITE; PSOL042; ZLUR PROFINESE; 1.
Rydrolame; Metalloproceses; Zinc; Signal; Glycoprocein; Zymogen;
Rydrolame; Metalloproceses; Zinc; Signal; Glycoprocein; Zymogen; PROSITE; PROSES, CYSTEINE SWITCH; FALSE NEG-PROSITE; PRO0427, DISINTEGRIN 1; FALSE NEG-PROSITE; PSS0214; DISINTEGRIN 2; FALSE NEG-Pfam; PF01562; Pep_M12B_propep; 1. Pfam; PF01421; Reprolysin; 1. SMRRT; SW00209; TSP1; 11. PROSITE; PS50215; ADAM MEPRO; 1

ADAMTS-9. METALLOPROTEASE POTENTIAL 1935

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1445 WSTGPWSSCSVSCGRGHKQRNVYCMAKDG-SHLESDYCKHLAXPHGHRKCRGGRC 1498

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MEROPS, M12.025; -. Genew, HGNC:16305; ADAMTS15.

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ADAMTS-15. METALLOPROTEASE. DISINTEGRIN-LIKE. TSP TYPE-1 1. POTENTIAL. BY SIMILARITY.

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CC or send an email to license@isb-sib.ch).
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ADANTS-20 Peterspoor [E. 3.4. Last annotesion update)

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                                                                                                                                                                                              1 WHVGTWMECSVSCGDGIQRRRDTCLGPQAQAPVPADPCQHLPKPVTVRGCWAGPC 55
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J. Stock Communication of ADAMTS-3 (2003) 5213 (2003).
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Asmmālia; Buthoria; Primates; Catarrhini; Rominidae; Homo.
KVGE_TRAID=6066;
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         DB 1; Length 950;
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Query Match 33.7%; Score 116.5; DB 1; Length 95 Best Local Similarity 41.8%; Pred. No. 8.6e-06. Metches 23; Conservative 5; Masmatches 24; Indels
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Event-Alternative splicing; Named isoforms=2;
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MEDLINE-22566039; PubMed=12562771;
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Memmila; Butherta; Primates; Catarrhini, Hominidae, Homo.
NGBI_TAXLE=5006;
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Pred. No. 3.7e-05;
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WHYGTWMECSYSCODGIORRRDTCLGPQAQAPVPADFCQHLPKPVTVRGCWAGPC 55 23; Indels 5; Score 101.5; DB 1; Length 1205; Pred. No. 0.00056; 6; Mismatches 38.2%; Best Local Similarity 38.2 Matches 21, Conservative Query Match

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Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Memmalia; Butheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus

Mus musculus (Mouse) NCBI_TaxID=10090; SEQUENCE FROM N.A.

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-! - PTM: The precursor is cleaved by a furin endopeptidase (By

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Bukaryota; Metazoa Chordata; Craniata; Verrebrata; Buteleostoni; Mamalia; Eutheria Rodentia; Schurognathi; Muridae; Musimae; Musi SEQUENCE FROM N.A.

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Raha S.S., Loquellano N Bosak S.A., McEwan P.J. Richards S., Worley K.C. Villalon D.K., Muzny D.	Fahey J., Helton B., Ke Whiting M., Madan A., Y Blakesley R.W., Touchma Rodriguez A.C., Grimwoo	Butterfield Y.S.N., Krzywins Schnerch A., Schein J.E., Jo "Generation and initial anal and mouse only semiences":	Proc. Natl. Acad. Sci. -1- FUNCTION: Cleaves to to fibril assembly.	play a role in deve collagen biosynthes -!- CATALYTIC ACTIVITY: alpha-1(I) at Pro-

nds 1 zinc ion per subunit (By similarity).
belong to a multimeric complex. Binds specifically to xxx (By similarity).
ACATION: Secreted. Associated with the extracellular

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peace docain and the TSP type-1 domains are important
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RESULT

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ADAM MEPRO, 1. DISINTEGRIN 1, FALSE NEG. DISINTEGRIN 2, FALSE NEG. AM46455.1; ... 6; Adamta2. 1052; Disintegrin. 1052; Pept M. Zn. 88. 1190; Peptidase M12B. 2270; Peptidase M12B. sprolysin; 1. 3AC30572.11 -.

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toprotease; Zinc; Signal; Glycoprotein; Zymogen;
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"Characterization of Anwirist, a novel member of the ADMRTS
injohim. Stocky, Acta 15721-225 (2001). Homo sapiens (Human)

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264 WYTGPWGECSSECGSGTQRRDIICVSKLGTEPNVTSPSN-CSHLPRPPALQ-----PCQG 317
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euleleostomi;
Mammalia; Datheria, Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                SEGURNES FROM N. N. 22. OX. T., Zhou X.M., Jiang H.O., Zhang P.P., Qin N.Y. Kan D. Y. X., Oxin X.W., Chan L.F., He L.P., Li H.N., Yu Y., Yu U., Hang Y., Qix X.W., Chan L.F., He L.P., Li H.N., Yu Y., Wan L.H., Whyeld Human CDNA clones with function of inhibiting cancer cell growth.
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41.0%; Pred. No. 2.8e-07;
tive 7; Mismatches 20; Indels 9;
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Mammalia; Butheria; Primates; Catarrhini; Hominidas; Homo
WCBI_TaxID=9606;
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SMBL, AP217974; AAG17217.1; -.
Genew, HGNC:19706; TSRC1.
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SBOURNCE 237 AA, 25659 MW, FB73ED571107026C CRC64;
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Matches 25, Conservative
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SMART; SM00209; TSP1; 3.
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Q8N643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1076 WHYGTWARECSYSCODGIQRRRDTCLOPQAQAPVPADFCQHLPKPVTVRGCKAGPCVGQ 1133
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                                                                                                                                                                                                                                                                                                                             O; Gabs
                                                                     VON WILLBBRAND FACTOR-CLEAVING PROTEASE
fW; EBIBC3AABCIA442 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-468-2010 (TEMBELGE), 15, Last sequence update)
01-667-2010 (TEMBELGE), 15, Last sequence update)
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                                                                                                                                                                                                                Query Match 100.0%; Score 346; DB 4; Length 1427; Best Local Samilarity 100.0%; Fred. No. 46-25; Machae 98; Conservative 0; Macatches 98; Conservative 0; Indels 0
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01-MAR-2003 (TrEMELrel. 23, Last amoreation update)
01-CCT-2003 (TrEMELrel. 25, Last amoreation update)
                                                                                                                                 153632 MW;
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InterPro IPR007110, Ig-11ke.
InterPro IPR003598, Ig. 62.
InterPro IPR003598, TSP1.
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                                                                                         75 1427
1427 AA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; PT0566; PT0566
PIR; PT0633; PT0633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=10090;
                                                                                         CHAIN
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6

Gaps

VAN-2000 (TEMBERE), 22 Creeted 01-WAN-2000 (TEMBERE), 23, Last sequence update) Mypotherical protein 24, Last amnotation update) Mypotherical protein 24, Last minotation update) Mus musculus (Mouse).

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                                                                             688 WHAGPWKPCTAACGRGLOSRKVDCIHTRSCKPVAERHCVOKKKPVSWRHCLGPSC 742
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1 WHYGTWARCSVSCGDGIQRRRDICLGPQAQAPYPADFCQHLPKPYTVRGCWAGPC 55
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Bukaryota; Metazot
Mammalia, Bultalis, Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Submitted (Nor-1999) to the PBM/Gensent/Deb database.

Interfer (Animals of Animals                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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42.9%; Pred. No. 2.2e-06;
ive 7; Mismatches 23; Indels
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11-MAx-2003 (TrEMBLrel. 23, Last sequence update)
11-GCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrENBLrel. 13, Last sequence update)
01-MAY-2003 (TrENBLrel. 24, Last annotation update)
Hypothetical protein (Fragment)
DKFZPA341204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     898 AA
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Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UFZ4
Q9UFZ4;
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                                                                                                                                                                                                                                                                                                                                 Bikkaryota, Mesazoa, Chordata, Cranasta, Vertebrata, Duteleostoal;
Mammalia, Ethesia, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
V(BLTMIDE)0990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mypothercal profess.

Monose fascicularis (Crab esting macaque) (Cymonolgus monkey).

Mokaryos, Messos, Chordats, Cranists, Verebrats, Buteleostoni,
Mammalis, Butheria, Primates, Christini, Ceropitherides

Ogrophiconise; Macada.
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Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
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RESULT 6

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SEQUENCE FROM N.A.

34.1%; Score 118; DB 6; Length 761; 36.4%; Pred. No. 1.9e-06; 11ve 8; Mismatches 27; Indels

Local Similarity 36.4 ses 20; Conservative

Query Match Best Loca Matches

| Signature | COT-2001 | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot | Cot |

35.4%; Score 122.5; DB 11; Length 701; 43.6%; Pred. No. 4.6e-07;

C854E56D0704805F CRC64;

Pfam; PF00090; tsp 1; 8.
SMART; SM00209; TSP1; 8.
PROSITE; PS50092; TSP1; 8.
Hypotherical protein.
SEQUENCE 701 AA; 77924 MW;

25; Indels

5; Mismatches

Matches 24; Conservative

Query Match Best Local Similarity

5

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Best Local Similarity
Matches 24; Conserve
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Best Local Similarity
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75 WFTGPWSECSSECGSGTQHRDIICVSKLGAEFNVTSPSN-CSHLPRPPALQ-----PCQG 128
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STRANN-CSTBL/G1.
MEDINE-2253009; PubMed-12706885;
MEDINED D.A., Medaler M.I.
"TSRCI, a widely expressed gene containing seven thrombospondin type I
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34.01; Score 117.5; DB 11; Length 1092;
selet Local Similarity 36.41; Per 66; No. 31:6-05;
Matches 20; Conservative 7; Wismatches 71; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  823 WSPSPWSQCSKTGGRGVRRREVLCKSPAAET-LPESLCSSSPRPEAQEGCVLGRC 876
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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33.74, Score 116.5, DB 11, Length 235;
Sest Local Similarity 39.34, Perd. No. 8.98-07;
Matches 24, Conservative 6, Mismarches 22, Indels 9;
PERMINENCIA (FEB. 12.)
PRINTS, PROLING; FEB. 12.
PRINTS, PROLING; FEB. 12.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.7%; Score 116.5; DB 13.
39.3%; Pred. No. 3.9e-06;
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PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
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EMBL, AF227652, AAKISO41.1; --
InterPoor : PRGM, PRGM, PRGM, PRGM, PRGMOSO9, TSD1, 7, SMART, SMOOZO9, TSD1, 5, SMOCZIE, PSGMOSO9, TSD1, 5, SMOCZIE, PSGMOSO9, TSD1, 5, SMOCZIE, PSGMOSO9, TSD1, 5, SMOCZIE, SMGMOSO, TSD1, 5, SMGMAL
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482
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AA;
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SEQUENCE
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095428
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                                                                      1 WHYGTWMECSVSCGDGIQRRRDTC-LGP-----QAQAPVPADFCQ----HLPKPV 45
        7, Mismatches 14; Indels 12; Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates; Catarrhini, Hominidas, Homo.
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Fighther as a member of a new family with smallarities to ADAN-TS
Functin, a member of a new family with smallarities to ADAN-TS
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33.2%; Score 115; DB 4; Length 1023;
Best Local Similarity 34.5%; Pred. Ro. 6e-06;
Matches 19; Conservative 8; Mismatches 28; Indels
Matches 19; Conservative 8; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases-1- SIMILARITY: CONTAINS 6 TSP TYPE-1 DOMAINS.
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OBULLY, ORTHONORY, PRT, 1023 AA.
OBULLY, ORTHONORY, PRT, 1023 AA.
OB. -AAY-2000 (TREMELAEL 13, Last sequence update)
OB. -CAT-2010 (TREMELAEL 13, Last sequence update)
TREMELAEL 25, Last sequence update)
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PRELIMINARY; PRT, 766 AA.
PP23997
D1-3704-2001 (TEMBLEE] 117, Created
D1-3704-2001 (TEMBLEE] 117, Last sequence update)
D1-3704-2003 (TEMBLEE] 23, Last annocation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADAM-TSL3 precursor (Fragment).
        24; Conservative
                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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        Matches
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510 WHVGTWGLCSKSCSSGTRRRQVICAIGP --- PSHCGSLQH-SKPVDVEPCNTQPC 560
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Query Match 32.84; Score 113.5; DB 4; Length 417; Best Local Similarity 42.14; Pred. No. 3.69-0.7 [Adels 5; Gaps Matches 21, Conservative 8; Mismatches 20; Indels 5; Gaps

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Search completed: March 13, 2004, 07:43:20 Job time : 6.73958 secs

20 12 20 12 12 12 12 12	AlideBhys SESUL 1 AlideBhys AlideBhys D MADidels membard; procein; 1297 AA.		PR 0-NOW-2002 (2004)-0-10-0-14-1. PR 3-APR-2002 (2004)-0-10-0-14-1. PR 3-APR-2002 (2004)-0-10-0-14-1. PR 3-APR-2002 (2004)-0-10-0-14-1. PR 3-APR-2002 (2004)-0-0-10-0-14-1. PR 3-APR-2002 (2004)-0-0-10-0-14-1-1-1-1-1-1-1-1-1-1-1-1-1-1
Copyright (0) 1993 - 2004 Compugen Ltd. OW procein earch, using as model 1991 - 2004 (0) 1992 - 2004 Compugen Ltd. March 13, 2004, 07:28:59 - 56e4 Compugen Ltd. 190-20-20-20-20-20-20-20-20-20-20-20-20-20	Midimum DB med_leaght, 0 Meximum DB med_leaght, 2000000000 Post_processing: Wilsiam Macch 04 Liteling first 45 summaries	Database: A	Comparison

Sequence 1297 AA

AAE24449 standard; protein; 1353 AA

RAE24449

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                                                                                                                                                                                                                                                        Human; Von Willebrand Eactor-cleaving protease; VWF-cp; therapy; enzyme;
                                                                                                                                                                                                                                                                                        treangent or animal; simination trivendoemolis disease; preeciampsis;
Etimonolis thromboytic purpura TTP; Hencch-Schoolish purpura,
Etimonolish nootasi I triemboytopaenia; haemolytic-uraemic syndrome;
Etimonolish anticoagulant.
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100.0%; Pred. No. 4.2e-32;
ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              weeming b, Gerritsen HE, Furlan W, Turecek P, Schwarz R;
Scheiflinger F, Antoine G, Kerschbaumer R, Tagläavacca L;
Simmermann K, Voelkel D;
                                                                                                                                                                                  Human Von Willebrand factor-cleaving protease fragment #2.
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12-APR-2001: 2001US-00833328
                                                                                                            (first entry)
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Matches 58; Conserv
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                                                                                                            04-OCT-2002
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                                      AAE24449;
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orn %liebrand factor-cleaving enzyme; thromboylogehic purpura;
myocardia infarcin; cerebral infarcion; arterioscierosis;
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4.1e-32;
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llarity 100.0%; Pred. No. 4.1e-32;
Conservative 0; Mismatches 0;
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                                                                                                                    0, Mismatches
                                      Score 346,
Pred. No. 4
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                               100.0%;
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2001JP-00302977.
2002JP-00017596.
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       Query Match
Sest Local Similarity 100.v
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N-PSDB; ABT32586.
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es 58; Conserv
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25-APR-2001:

27-JUL-2001; 25-JAN-2002;

Soejima K,

Homo sapiens

07-NOV-2002

15-MAY-2003

AA016620:

90

Gaps

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AA016617,

Query Match

RESULT

(first entry)

15-MAY-2003

WO200288366-A1.

07-NOV-2002

25-APR-2001;

Homo saplens.

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The invention comprises the matto exist and coding squence of a von Willabeard stateor (very)-cleaving energyes. The DNA and protein sequences of the invention are seated in it has disponsible and treatment for cities introduced properties part in the disponsible and treatment of cities. The protein comparison to the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the
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/note= "The mature form of the ADANTS-M protein is
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100.0%; Pred. No. 4.3e-32;
ive 0; Mismatches 0;
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27-JUL-2001; 2001JP-00227510.
28-SEP-2001; 2001JP-00302977.
25-JAN-2002; 2002JP-00017596.
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58; Conservative (
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                                                     07-NOV-2002
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                                                                                                                                                                Human von Willebrand factor (vWF)-cleaving enzyme-related protein #4.
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                                                                                                                                                                                                                                                     Human, protease inhibitor; gene therapy, vWF-cleaving enzyme;
or Wilebrand sector-cleaving enzyme; thromborycopinic purpura;
myocardia infarction; cerebral infarction; arterioscierosis;
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100.0%; Pred. No. 4.2e-32;
iive 0; Mismatches 0; Indels 0
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28-SEP-2001; 2001JP-0032977.
25-JAN-2002; 2002JP-00017596.
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Mimura N, WPI; 2003-120479/11.

Soejima K,

N-PSDB; ABT32583.

15-MAY-2003 (first entry)

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W0200288366-A1 domo sapiens.

Conservative

Local Similarity Hes 58; Conserv Seguence 1353 AA,

Query Match

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89 Gaps

	рошаіп	Domain	Domain	Domain	Domain	Domain	EP11520	07-NOV-	24-APR-	27-APR-	(BEIZ)	Bụckbin	WPI, 20 N-PSDB;	New pol	transpl encoded	Claim 4	The pre	that ex	thrombo	compris	prodoma	and age	polynuc	rheumat	asthma	breast.	Leukaer	spinal	multip	diabet	-
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vnucleoride, useful in gene therapy, particularly for treating or ing e.g. arthritis, Crohn's disease, Alinesmen's disease and organ ant toxicity and rejection, comprises ADAMTS polynucleoride and polypeptide. processed by furin cleavage of the prodomain" Wachtmann TS, Walsh RT; 110. .473 Tabel= Thrombospondin submotif 19. .424 label= Heparin-binding_domain 099. .1156 label= Thrombospondin_submotif label= Metalloprotease domain label= Disintegrin domain .abel= Zinc-binding_motif Fig 2; 31pp; English 2001; 2001EP-00303706. 2000; 2000US-0200040P. der L, Mitchell PG, 394 PPIZER PROD INC 02-084275/12. ABA02549. 55-A1

Nuntington's disease, Parkingon's disease, migraine, pain, depression, multiple scleracia, abnormal vouch hallongo, Durn, intertity or disheric motor, The polymuleonide and polymeptide are also useful for dispersions the flowesses abnorm. The polymuleonide are later useful in sene interests abnormal the particularly useful in sene interesty for treating the diseases above cited above.

Sequence 1416 AM;

ch 100.0%; Score 346; DB 5; Length 1416; Isiniarity 100.0%; Pred. No. 4.5s-32; Indels 0; Gaps 58; Conservative 0; Minnaches 0; Indels 0; Gaps Best Local Similarity Matches 58; Conserv **Duery Match**

Human; Von Willebrand factor-cleaving processor vertex, thretpy; surpre-training fire and in Termination; thromboembolic disease; presciampsis, thrombolic thromboryto puppus; TPP; Manoch-Schoulsin purpurs; thrombols; membrand introductopements; hamonlytic-ursestic syndrome; trainingentic; anticlosegulant; chromosome 9. Human Von Willebrand factor-cleaving protease (vWF-cp) note= "Mature human vWF-cp protein" 'note= "Thromspondin type I motif" [41. .553 note= "Thromspondin type I motif" note= "Thromspondin type I motif" 1016. .1073 /note= "Thromspondin type I motif" 'note= "Thromspondin type I motif" note= "Thromspondin type I motif" note= "Thromspondin type I motif" "Distintegrin like motif" "Cysteine rich region" note= "Furin cleavage site" 24. .228 notes "Catalytical side" label= Signal peptide AAE24450 standard; protein; 1427 AA. Location/Qualiflers "note= "Met turn" "Spacer" .1013 'note= "Sp 588. .743 (first entry) 439 .687 . 805 . 952 1427 75 "note" notes Cleavade-site Homo sapiens 04-OCT-2002 AAE24450: Peptide Protein Domain Comain Domain. Domain lomain. Region Region Domain Domain Region Domain AE24450

W0200242441-A2

10-NOV-2001; 2001WO-EP013391 22-NOV-2000; 2000US-00721254 12-APR-2001; 2001US-0083328 30-MAY-2002

BAXT) BAXTER AG.

laemmie B, Gerriteen HB, Furlan M, Turecek P, Schwarz H; Schneffligeer F, Antolne G, Kerschbaumer R, Tagliavacca L; Voelfell Woelfel

WPI; 2002-479950/51. N-PSDB; AAD39332.

Novel isolated or substantially purified von Willebrand factor-cleaving processes, useful for producing preparation for therapy of thrombosis and thrombosicalic disease auch as thrombotic thrombotytic purpurs.

Claim 1, Fig 5, 93pp; English

ch 100.0%; Score 346; DB 5; Length 1427; Similarity 100.0%; Pred. No. 4.5e-32; S8; Conservative 0; Mismatches 0; Indels 0; Local Similarity Matches

ADD94038

Human aggrecanase protein amino acid seguence. 29-JAN-2004 (first entry)

human; enzyme

Home sapiens

US2003105313-Al

Agostino MJ, Wolfman N, Morris EA; (AMHP) AMERICAN HOME PROD CORP. Racie LA, Twine NC,

WPI; 2003-801251/75. N-PSDB: ADD94037.

The invention of release to an aimstand or materiarilly preto factor-(dawing processe (VMF*Cp) tolympide, WMF*Cp is useful for
the processe of the invention

Sequence 1427 AA;

1 MHVGTMMECSVSCQDGIORRRDTCLGPQAQAPVPADFCQHLFXPVTVRGCMAGECVGQ 58 0; Indels 0; Gaps

1076 WHYGTWMECSVSCGDGIQRRRDTCLGPQAQAPVPADFCQHLPKPVTVRGCWAGPCVGQ 1133

ADD94038 standard; protein; 1427 AA.

aggreenames: aggreent, strictists extilage; protecylytis; centraling degradation; operoarthitis; inflammatory obint disease; andtarthitis; operoarthitis; inflammatory obint disease; andtarthitis; operoarthitis; inflammatory condition;

05-JUN-2003

25-JAN-2002; 2002US-00057487. 16-OCT-2001; 2001US-00978979

New isolated DNA molecule exceding an aggrecanase polypeptide for producing a purified human aggrecanase protein which can be used to develop infultors of aggrecanase. Claim 14; SEQ ID NO 8; 24pp; English. This invention raless to a novel haws appearance potent and the DNA sequence which encodes it. Aggreen is a major extractibilat component of actious continge. It is professybuse regionate for providing cartilage with its mechanical properties of compressability and adjacticity. A proceleyfur entryity forgermane's is repossable for the cleavage of aggreen insetby having a role in cartilage degradation

senceited with descentities and inflamentory joint disease, compound which inhibit the scriity of the present of the invention may have andicathicities casepainted or mainfallamentory activity. The livention may be used to produce a purified human appressment procein. The growth the administration of the produce a purified human appressment procein. The growth the disease and the procein and any act of the procein and any act of the procein and any act of the procein and any act of the procein and any act of the procein and appressment as used to inhibit the procein and the any act of the procein and appressment and the procein and appressment and the procein and appressment and appressment and appressment and appressment appressment and the human appressment appressment (full length sequence) of the invention.

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ch 100.04; Score 346; DB 7; Length 1427; LSimilarity 100.04; Pred, No. 4.5e-32; Drindels 0; Sels, Conservative 0; Mismarches 0; Indels 0; Best Local Similarity Sequence 1427 AA;

Query Match

1076 WHVGTWMECSVSCGDGIQRRRDTCLGPQAQAPVPADFCQHLPKPVTVRGCWAGPCVGQ 1133 1 WHYCTWARCSVSCGDGIQRRRDICLGPQAQAPVPADFCQHLDKRVTVRGCWAGPCVGQ 58 Gaps Matches

RESULT 9 ABB98125

ABB98125 standard; protein; 1445 AA. ABB98125;

Human PNPM Incyte ID 7473607CD1 17-OCT-2002 (first entry)

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domo gapiens

40200246383-A2 L3-JUN-2002 DS-DEC-2001; 2001WO-US046964.

08-DEC-2000; 2000US-0254399P. 21-DEC-2000; 2000US-025003P 05-JAN-2001; 2001US-0260110P. 19-JAN-2001; 2001US-026281P. 25-JAN-2001; 2001US-0264623P. (INCY-) INCYTE GENOMICS INC Azimzai Y, Kallick DA, Baughn MR, Griffin JA, Swarnakar A; Malla MK, Hefalia AJA, Gendhi AB, Aur'Sonng J, Elliott V9; r J, Thngavelu, Lu Y, Marren BA, Lu DM, Lee EA; ey CM, Arvin C, Delegenne AM, Yeo MG, Khan FA; Tribouley CM, Sanjanwala MM, Lal pG, Wal Ramkumar J, 'ue E'

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Query Match
Best Local Similarity 100.0
Matches 58; Conservative
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  WPI; 2002-519664/55.
N-PSDB; ABQ75946.
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New isolated Protein Modification and Maintenance polypeptides, useful for diagnosis, and treatment of e.g. gastrointestinal disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 346; DB 5; Length 1445; 100.0%; Pred. No. 4.6e-32; ive 0; Mismatches 0; Indels 0;
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                                                                                                      laim 1 (a); Page 154-157; 200pp; English
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77 WYTGPWGECSSEGGGTQRRDIICVSKLGTEFNVTSP8N-CSHLFRPPALG-----PCGG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The inventor comprise the aims out of an ording separate of those process. The NAM and process against on the inventors are swell as precise, the NAM and process against on the inventors are said to the inventors and inventors are said to the inventors and inventors are said to the inventor or again to a family formerower market or again to family formerower and to map a falled game golfflows make to comprete that made from the management of the family and to a semplification of the family and to the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the family and the admitstantian of the admitstantian of the family and the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian of the admitstantian
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Wang Z;
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chromosome marker; genetic disorder; contig.
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g G, Zhou P, Drmanac RT,
such as cancer. The present sequence represents a human cancer suppressing protein from the present invention
                                                                                                                                                                                                                                            Length 237;
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                                                                                                                                                                                                                        35.4%; Score 122.5; DB 5,
ilarity 41.0%; Pred. No. 2.3e-06;
Conservative 7, Mismatchem 20
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Shosh M, Xue AJ, Wehrman T, Weng G, 21
Xa Y, Wang D, Chen R, Xu C, Boyle BJ;
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12-SEP-2000;
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                                           9; Gans
    DB 7; Length 358;
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th 35.4%, Score 122.5, DB 7, Similarity 41.0%; Pred, No. 3.6e-06, 25; Conservative 7, Mismatches 20,
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Isolated polypeptide for treating, preventing and/ or prognosing medical disorders and also for testing and detection e.g. diagnosis and ecreening Claim 11; SEQ ID NO 45; 469pp; English Ruben SM

The Marker's Annual Structures and the correspondence to work of the Annual process of the Annual Process of the Annual A

DB 4; Length 372; Query Match 35.4%; Score 122.5; DB 4; Best Local Similarity 41.0%; Prod. No. 3.7e-06; Best Local Similarity 7; Mismatches 20;

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ADC22076 standard; protein; 372 AA

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.nflammatory disorder; proliferative disorder; Human

Homo sapiens.

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2000US-0209467P 2000US-0214886P 2000US-021513F 2000US-0216647P 2000US-0216880P 2000US-0216880P 2000US-0216880P

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14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

2000US-0225447P 2000US-0225757P 2000US-0225758P 2000US-0225759P 2000US-0227182P

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New nucleic acid molecules and polypaptides for disapposing, preventing or
creating disorders associated with aberrant expression of the
polypoptide, e.g. neural or cardiovacular disorders, and in chromosome
demitication.
                                                                                    Maim 11; SEQ ID NO 45; 242pp; English
Rosen CA, Ruben SM, Barash
                                                            HUMA- HUMAN GENOME SCI INC
                                                                   WPI; 2003-786903/74.
N-PSDB; ADC22050.
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       212 WYTGPWGECSSECGSGTQRRDIICVSKLGTEFNVTSPSN-CSHLPRPPALQ-----PCQG 265
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Seven nucleic acid molecules encoding ADAM polypopiides containing a distincepth and metalloprocesse domain, useful in the prevention, tractment and diagnosis of cancer, immine disorders, cardiovascular.

Hastings GA,

WPI, 2001-016507/02.

25-MAY-2000; 2000WC-US014308, 29-JUL-1999; 99US-0142930P. HUMA-) HUMAN GENOME SCI INC

27-MAY-1999;

WO200073323-A2

07-DEC-2000 09-JUL-1999 Ruben SM.

Homo sapiens.

ovarian.

Claim 11; Page 274-276; 287pp; English

Sisorders and neurological diseases.

disintegrin, metalloprotease; food additive, breast cancer,

ADAM protein #2

20-XAR-2001

AABS0936 standard: protein: 491 AA.

AAB50936

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1 WHVGTWMECSVSCGDGIQRRRDTC---LGPQAQAPVPADFCQHLPKPVTVRGCWAGPCVG

ABU60626 standard; protein; 491 AA.

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35.4%; Score 122.5; DB 4; Length 491; 41.0%; Pred. No. 5e-06;

therapy of breast and ovarian cancer

Mismatches

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331 WYTCHWARECSSCGSGGARDICVSKLGTERVVTSSR-GSHLRRPPLQ------DCOG 384

Search completed: March 13, 2004, 07:39:07 Job time : 9.48854 secs

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                                                   CURRENT APPLICATION NUMBER: US/10/222,334
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Patent No. US20020090674A1
GENERAL INFORMATION:
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publication No. US20030105313A1
GENERAL INFORMATION:
                                                                                                                                            PROCR APPLICATION NUMBER (0) 112
PRIOR FILING DATE 201 00-16
NUMBER OF SEA ID NOS: 78
SOFTWARE Recentin version 3.1
SEQ ID NO 2
LIBROTH: 1427
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SOFTWARE: Patentin version 3.1
SEQ ID NO 8
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US-10-057-487-8
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Best Local Similarity
Matches 25; Conservat
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US-10-222-334-2
                                                                                                                  CURRENT FILING DATE:
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US-09-764-903-45
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1 WHYGTWINECSVSCGDGIQRRRDTCLGPQA---QAPVPADFCOHLPK-PVTVRGC---- 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 19,
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15.4%; Score 122.5; DB 9; Length 645;

Best Local Similarity 38.2%; Pred. No. 1.46-05;

Metches 29; Conservative 6; Mismatches 22; Indels 19;

Metches 29; Conservative 6; Mismatches 22; Indels 19.
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APPLICANT Zerhusen, Bryan D.
APPLICANT Komuver, Leasto
APPLICANT Komuver, Leasto
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CURRENT APPLICATION NUMBER: US/10/087,887
TUTRENT FILING DETE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/273,049
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PRIOR APPLICATION NUMBER: 60/282,867
PRIOR FILING DATE: 2001-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 89, Application US/10087887
Publication No. US20030198957A1
GENERAL INFORMATION:
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SOFTWARE: CuraSequist version 0.1
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Yang, Ruey-Bing
Hart, Matthew
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 762
LENGTH: 645
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US-09-764-853-762
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SEQ ID NO 89
LENGIH: 56
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Matches 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WHYGTWMECSVSCGDGIORRRDTC---LGPQAQAPVPADFCQHLPRPVTVRGCWAGPCVG 57
                                                                                                                                                                                                                                           Score 122.5; DB 13; Length 491;
Pred. No. 1.1e-05;
7; Mismatches 20; Indels 9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING BATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF EED ID NOS: 339
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PRIOR PILLING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/142,930
PRIOR PILLING DATE: 1998-07-09
PRIOR PILLING DATE: 1998-07-09
PRIOR PILLING DATE: 1999-05-27
SPECOR PILLING DATE: 1999-05-27
SOFWARE OF SEQ ID NOS: 2.0
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Patent No. US20020090672A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/10125452
Publication No. US20020173640A1
                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 41.0%;
Matches 25; Conservative
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                                        TYPE: PRT
, ORGANISM: Homo sapiens
US-10-125-470-10
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          LENGTH: 491
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US-09-764-903-46

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Score 121.5, DB 9; Length 367,
Pred. No. 1.18-05;
9; Mismatches 24; Indels 1; Gaps
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15.14, Score 121.5; DB 9; Length 369;
Best Local Similarity 38.24; Fred. No. 1.1e-05;
Matches 21; Conservative 9; Mismatches 24; Indels 1)
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NUMBER OF SEQ ID NOS: 67
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TITLE REFERENCE: 21402-240
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Percent No. US2002009674A.
GENERAL INFORMATION NAME OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PROJECT OF A PR
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CTREARY PRINCIPATION DAYS

PRICIO APPLICATION DAYS

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CURRENT FILING DATE: 2001-01-17
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Publication No. US20030203843A1
GENERAL INFORMATION:
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APPLICANT: Guo, Xiaojia
APPLICANT: Shimkete, Richard
APPLICANT: Paddgaru, Muralidhara
APPLICANT: Rekuda, Ramesh
                                                                                                                                              35.1%;
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Edinger, Shlomit
Smithson, Glennda
Gunther, Erik
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Mehraban, Fuad
Topper, James N.
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Wasserman, Scott
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SEQ ID NO 43
LENGTH: 369
                                                                                                                                              Query Match
Best Local Similarity 38.21
Matches 21, Conservative
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US-09-764-903-43
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US-09-764-903-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 WHVGTWMBCSVSCGDGIQRRRDICLGPQAQAPVPADFCQHLPKPVTVRGCWAGPC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
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                                                                                                                                                                                                                                                                 PRICIONT: ORDER THE B.
APRICIONT: ORDER THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PRICE THE PR
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TITLE OF INVENTION Nucleic Acids, Proteins, and Antibodies FILES REPERBNCS: P728
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CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/273,049
PRIOR FILING DATE: 2001-03-02
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PERCOR PLEATER TOWN
Sequence 16, Application US/10087887
Publication No. US20030198957A1
GENERAL INFORMATION:
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Patent No. US20020090674A1
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 16
LENGTH: 283
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ORGANISM: Homo sapiens
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LOCATION: (168)
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LOCATION: (226)
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US-09-764-903-46
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APPLICARY: Ellerant, Marchi, Marchi, Marchine Colypop
THILD OF INVESTIONS NO. USCOGNODESSEARCH Antibodies that Bind to Antigenic Polypop
FILE REFERENCE: 2140-2777
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PRIOR FILTING DATE: 2010-66-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEO 10 NGS: 299
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35.1%; Score 121.5; DB 15; Length 1162; Best Local Similarity 38.1%; Pred; No. 328-05; Matches 21; Conservative 9; Wismatches 24; Indels 1; Matches 24; Lindels 1;
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                                                                                                                 35-10-16-493-124
Sequence 124 Application US/10:61493
Sequence 124 Application US/10:61493
GRARBAL INFORMATION:
APPLICANT: Arderson, David W
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Taupier Jr., Reymond J
Guo, Xiaojia Sasha
Miller, Charles E
Shenoy, Suresh G
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Voss, Edward Z
Boldog, Ferenc L
Malyankar, Uriel M
Padigaru, Muralidhara
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Gerlach, Valorie
Shinkets, Richard A
Gorman, Linda
Pena, Carol EA
Kekuda, Ramesh
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Smithson, Glennda
Edinger, Shlomit R
Millet, Isabelle
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Spytek, Kimberly A
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Li, Li
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Rastelli, Luca
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US-10-161-493-124
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LENGTH: 1162
TYPE: PRT
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Pred. No. 3.2e-05;
9; Mismatches 24; Indels 1; Gaps
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Publication No. US20030203843A1
GENERAL INFORMATION:
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Sequence 15, Appl.
Sequence 27, Appl.
Sequence 5, Appl.
Sequence 5, Appl.
Sequence 12, Appl.
Sequence 12, Appl.
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US-09-429-116-3
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                     US-08-313-288B-19

US-08-313-288B-20

US-08-313-288B-20

US-08-35-364A-7

US-08-95-56-3

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Patent No. 6605592
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GENERAL INFORMATION:
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RESULT 2
       Sequence 16, App
Sequence 16, App
Sequence 172, App
Sequence 21, App
Sequence 21, Appl
Sequence 17, Appl
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Sequence 13, Appl
Sequence 15, Appl
Sequence 155, Appl
Sequence 15, Appl
Sequence 171, Appl
Sequence 111, Appl
Sequence 113, Appl
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Regult No.

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OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
JURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
JS-09-800-729-165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ni et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IS-09-491-522-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GOLCARA, FOUR STATEMENT GOODSTAT, AND TANGO-73, TANGO-74, TANGO-76, AND TANGO-83 FITTLE OF INSPENCE. PARAGO-11, TANGO-73, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TANGO-74, TAN
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Pred. No. 1.2e-05;
8; Mismatches 24; Indels 1;
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Pred. No. 8.4e-06;
6; Mismatches 25; Indels 3
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VENTION: 32 Human secreted proteins
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BARLIER FILING DATE: 1997-08-06
SOFTWARE: PESCENG for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FLIKE DAFE: 1986-09
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 155, Application US/09800729
Patent No. 6605592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09130491
Patent No. 6416974
GENERAL INFORMATION:
                                                                 ORGANISM: Homo sapiens ADAMTS-9
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Best Local Similarity 40.0%;
Matches 22; Conservative b
                                                                                                                   NAME/KEY: MOD RES
LOCATION: (46B)
OTHER INDORMATION: Xaa = C
NAME/KEY: MOD RES
LOCATION: (52\overline{1})
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Best Local Similarity 39.34
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa = Y
US-09-369-364A-13
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LENGTH: 1882
TYPE: PRT
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                                                                                                     FEATURE
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1371 WATGPWIACSATCGNGTORKLIKC--RDHVRDLPDEYCNHLDKEVSTRNCRLRDC 1423
                                                                                                                           1 WHYGTWARCSVSCODGIQRRRDICLGPQAQAPVPADPCQHLPKPVTVRGCWAGPC 55
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Pred. No. 7e-06;
                                 Query Match 32.4%; Score 112; DB 4; Length 2165; Best Local Similarity 38.2%; Pred. No. 0.0011. Matches 21; Conservative 6; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6
                                                                                                                                                                                                                                                                                                                                                                     ON: 32 Human secreted proteins
PZ044P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PZ044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MBER: PCT/US00/26013
2000-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60/155,709
                                                                                                                                                                                                                                                                                    Sequence 165. Application US/09B00729
Patent No. 660552
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09491522
Patent No. 6428998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-09-24
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Best Local Similarity 42.6%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FICE APPLICATION NUMBER:
FICE FLING INFE; 2000-09-
FRICE FLING INFE; 2000-09-
FRICE FLING INFE; 299-09-
NUMBER OF SEQ ID NOS: 217-
SOOFMARE: Petentin Ver: 2.05
US-09-800-729-155
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Gaps

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296 WEAGKWSKCIASCGGGVRRRHVACVG-----GSDCDEGGRPRQETICYAGIPC 343
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                                                                                                                                                                                                                                                                Query Match 29.3%; Score 101.5; DB 4; Length 56; Best Local Similarity 33.3%; Pred. No. 3.8e-95; Matches 19; Conservative 7; Manatches 29; Indels 3; Matches 19; Conservative 7; Pred. No. 200.8e-79.
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Patent No. 6605592
GENERAL INFORMATION:
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Parent No. 6391610
GENERAL INFORMATION:
APPLICANT: Aprc. Suncel
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APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
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Patent No. 6605592
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Pred. No. 0.00024;
5; Mismatches 10; Indels
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3174 Porter Dr.
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US 60/225,852
PRIOR PILING DATE: 2000-08-16
PRICE FILMS OATS: 2000-09-22
PRICE APPLICATION NUMBER: 60/155.709
PRICE FILMS DATE: 1999-09-4
SOFTWARE OF SEQ ID NOS: 217
SOFTWARE PERFELL VEF. 2.0
LENGTH: 60
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Patent No. 5876963
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Patent No. 6448388
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Best Local Similarity 30.9%;
Matches 21; Conservative 5
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APPLICANT: Friddle, Carl Johan
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CORRESPONDENCE ADDRESS:
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US-09-800-729-167
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LENGTH: 1224
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US-09-930-872-4
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                                                                                                                           Sequence 16: Application US/OSB00729
PRESENT NO. 660592
GREEKLAIN HISOMATION 1.3
PRESENTE TO PROVE HIS COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF THE COUNTY OF T
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Patent No. 660592
APPLICANT, NI et al.
TILL OF INVENTION: 12 Human secreted proteins
FILL SEPERANCE: PSC04491
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APLICANT: NI et al.

TITLS OF INVENTION: 32 Human secreted proteins
FLES RETREMENT POOL 471

COURSAN APLICATION BUNGER: US/09/800.729

CURRAY FLEINO PIER: 2001-02.02
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CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
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Patent No. 6605592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1999-09-24
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PRIOR FILING DATE: 1999-09-2
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PATENTIN VET: 2:0
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 34.5%
Warches 20; Conservative
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ORGANISM: Homo sapiens
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US-09-800-729-124
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US-09-800-729-167
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                                                                                                  US-09-800-729-169
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LENGTH: 514
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Prov. March 26, 94, Score 59, 10 B 2, Length 788; Best Local Smilerty 41.54, Pred. No. 0.0064, 10. 10. 0.0064, Marches 22; Conservative 4; Mismatches 15; Indels 12; Oaps Marches 22; Conservative 4; Mismatches 15; Indels 12; Oaps Conservative Conservation Conservative Conservation Conservati

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Search completed: March 13, 2004, 07:46:08 Job time : 2.44688 secs